# 10/649, 273

#### Swope, Sheridan

From:

Swope, Sheridan

Sent:

Wednesday, January 26, 2005 1:34 PM

To:

STIC-Biotech/ChemLib

Subject:

10/649,273

For 10/649,273, pls search and interference search:

SID 2, full-length, against the NT and AA data bases

SID 2, residues 148-414, against the NT and AA data bases

SID 2, residues 176-414, against the NT and AA data bases

Sheridan Swope, Ph.D.
Patent Examiner, AU 1652
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E02C70 Remsen Bld (Mailbox)



# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 143413

TO: Sheridan Swope

Location: REM-2B71/2C70

**Art Unit: 1652** 

Thursday, February 17, 2005

Case Serial Number: 10/649273

From: Mary Jane Ruhl

**Location: Biotech-Chem Library** 

Remsen 1-A-62

Phone: 571-272-2524

maryjane.ruhl@uspto.gov

### Search Notes

Examiner Swope,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl Technical Information Specialist STIC Remsen 1-A-62 Ext. 22524



### STIC-Biotech/ChemLib

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From:

Swope, Sheridan

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Sheridan Swope, Ph.D. Patent Examiner, AU 1652 Recombinant Enzymes 571-272-0943 (voice) E02B71 Remsen Bld (Office) E02C70 Remsen Bld (Mailbox)

STAFF USE ONLY

Searcher: \_\_\_\_\_\_Searcher Phone: 2Date Searcher Picked up: \_\_\_\_\_
Date Completed: \_\_\_\_\_
Searcher Prep/Rev. Time: \_\_\_\_
Online Tirne: \_\_\_\_\_

Type of Search

NA Sequence: #

AA Sequence :#

Structure: #

Bibliographic:

Litigation:

Patent Family:

Other:

Vendors and cost where applicable STN:

DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other(Specify):

# Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated

- accession number. permanent accession numbers. The new UniProt record may not contain the previous temporary numbers from the most recent version of UniProt. These sequences have been assigned new Please note that the curators of the UniProt database have purged some temporary accession
- accession number can be found by searching the old accession number in the UniProt Protein extension .rup) that can no longer be found in the database, the permanent record with the new If you encounter an accession number from an older search run against UniProt (results file Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher

numbers. members of the public who may encounter UniProt temporary accession include a copy of this attachment to assist any future Examiners or When submitting sequence search results for scanning into IFW, please Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

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Maximum
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# SUMMARIES

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# ALIGNMENTS

RESULT 1

### Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; immune disorder; retumatoid arthritis; acquired immunodeficiency syndrome; ALDS; pulmonary disease; pneumonia; emphysema; cystic fibrosis; vascular disorder; inflammatory disorder; neurological disorder. ABG96478 standard; protein; Novel human metalloprotease MP1. 11-DEC-2002 ABG96478; (first entry) 414 Å

Homo sapiens.

WO200272751-A2

19-SEP-2002.

05-FEB-2002; 2002WO-US003353

05-FEB-2001; 10-APR-2001; 2001US-0266518P. 2001US-0282814P.

(BRIM ) BRISTOL-MYERS SQUIBB CO.

WPI; 200 N-PSDB; 2002-723329/78. DB; ABS76635.

Chen

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Peder J,

Nelson TC,

Duclos

۳J •

Krystek

New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metallogroteinase activity, e.g. immune, metabolic, inflammatory and neurological disorders.

Claim 5; Fig 1A-C; 473pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a metalloprotease (MP-1). (I) is useful for preventing, treating, or

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cerebroprotective; antiparkinsonian; nootropic; antiinflammatory; antiulcer; hepatotropic; gynaecological; antibacterial; virucide; protozoacide; antiparasitic; cell proliferative disease; pMOD; protein modification and maintenance molecule; immunogenic fragme

autoimmune; inflammatory

disease; neurological

fragment,

Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; Human protein modification + maintenance molecule protein

anticonvulsant;

SEQ ID

ö

01-MAY-2003

(first entry)

ABJ26654 standard;

protein;

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RESULT 3
ABJ26654
ID ABJ2
XX
AC ABJ7
XX
DT 01-1
XX
DE Hum
XX
KW Cyt
KW Cer
KW cer
KW ant
KW pr(
KW pr(
KW Ca)
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMIAWNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THRAILFCKQRDLLFQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCFPPRLCTDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLHHAKNCDFSFTGLQHYTDKI IMKKEKEEGI EKGQI LSSAADI AATVQHTMACHLVKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALSIGVGLSFSLQLVGQLKKPFIPIHIMEAHALTIRLTNKVBFPFLVLLISGGHCLLALV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 2125; DB 5; llarity 100.0%; Pred. No. 2.2e-215; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
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The invention relates to an isolated polypeptide comprising: any of 28 CC sequences of 48-1256 amino acids; a natural amino acid sequence at least CC 90% identical to the 28 amino acid sequences, 94% identical to a sequence CC of 703 or 267 amino acids, 96% identical to a sequence of 414 amino CC the isolated polypeptide. The polypeptides and polymeclectides are useful CC in diagnosing, treating and preventing diseases or conditions associated CC with the decreased expression of protein modification and maintenance CC molecules (PMOD), such as cell proliferative diseases (e.g. Cancer, CC alterose), autoimmune/inflammatory diseases (e.g. AIDS, CC epilepsy), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g. CC epilepsy), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g. CC useful in assessing the effects of exogenous compounds on the expression CC useful in assessing the effects of exogenous compounds on the expression of funcleic acid and amino acid sequences of PMOD. The PMOD or its CC antegonist of the polypeptide, The microarray is useful in monitoring compounds that specifically bind to or modulate the activity of the polypeptide. The microarray is useful in monitoring or measuring protein increactions, drug-target interactions, and corrections.
                                                                                      Query Match
Best Local Similarity
Matches 414; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-2001; 2001US-0300508P.
06-JUL-2001; 2001US-0303445P.
13-JUL-2001; 2001US-03136405P.
09-AUG-2001; 2001US-0311442P.
24-AUG-2001; 2001US-0318921P.
29-AUG-2001; 2001US-0318992P.
03-MAY-2002; 2002US-0378205P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human PMOD polypeptide and polynucleotide, useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thangavelu K, -- WK, Mason PM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 63; Page 182-183; 225pp;
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                                                                                                                                                                                                                  Sequence 414 AA;
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                                                                                                                                                                                                                                                                                                        expression profiles. This sequence represents a human PMOD
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MLILTKTAGVPPKPSKRKVYBPLRSFNPHPGTLFLHKIVLGIBTSCDDTAAAVVDBTGNV
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                                                                                      Conservative
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, Gietzen KJ,
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                                                                                                               100.0%;
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                                                                                         0
                                                                                  Score 2125; DB 6;
Pred. No. 2.2e-215;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
                                                                                                                                            Length
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L, Yao MG;
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                                                                                  Gaps
                                                                                                                                                                                                                                                                                                        protein
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문 S

MLILTKTAGVFFKPSKRKVYBFLRSFNFHPGTLFLHKIVLGIBTSCDDTAAAVVDBTGNV

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ARESULT 4
ARE29234
ID ARE2
XX ARE2
XX ARE2
XX ARE2
XX ARE2
XX Huma
XX Huma
XX Huma
XX Freu
XX Crere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome mapping; tissue typing; gene therapy; neuroprotective; cytostatic; anorectic; cardiant; haemostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7TM; glycoprotease; immune disorder; IgA deficiency; allergy; arrhythmia; rheumatoid arrhritis; diabetes; atherosclerzosis; cardiovascular disorder; hypertension; ischaemic heart diseorder, obesity; myocardial infarction; endothelial cell disorder; Grave's disease; psoriasis; brain disorder; Parkinson's disease; Alzheimer's disease; haematopoietic disorder; cerebral oedema; metabolic disorder; liver disorder; platelet disorder;
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e= "Transmembrane domain"
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                                                                                                                                                                                      "Non-transmembrane domain; cytoplasmic
                           "Sialoglycoprotease type domain"
                                                                                "Non-transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel 38650, 28472, 5495, 65507, 81588 CC or 14354 nucleic acid molecules which encode adenosine deaminase, glyco-grotease or seven transmembrane domain (7TM) receptor family members.

CC Sequences of the invention are useful in diagnosing and treating cancer cor aberrant cellular proliferation and/or differentiation (e.g. colon or clung cancer), immune disorders (e.g. selective IgA deficiency, rheumatoid cor arthritis, diabetes, allergy), heart or cardiovascular disorders (e.g., hypertension, atherosclerosis, arrhythmias, ischaemic heart disease, cor myocardial infarction, thrombus) including endothelial cell disorders (e.g., psoriasis, Grave's disease), haematopoietic disorders, brain cor disorders (e.g. cerebral oedema, Parkinson's or Alzheimer's disease), cor disorders (e.g. cerebral oedema, Parkinson's or Alzheimer's disease), cor disorders (e.g. diagnostic disorders (e.g. obseity), liver disorders or platelet conditions and parkinson's and prophylactic and therapeutic methods. The concleic acids may also be used in chromosome mapping, tissue typing and corensic biology and as surrogate markers. Sequences of the invention are also used in gene therapy. The present sequence is human glycoprotease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules, useful for diagnosing and treating cancer, immune, cardiovascular, hematopoietic, brain, pain, metabolic, liver or platelet disorders, and
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08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 8; 178pp; English.
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                                                                          PPLHHAKNCDFSFTGLQHVTDKI IMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKR
                                                                                                                                                 QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK
                                                                                                                                                                                                                         ALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRLTNKVEFPFLVLLISGGHCLLALV 180
                                                                                                                                                                                                                                                                         LGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQEALSASGVSPSDLSAIATTIKPGL
                                                                                                                                                                                                                                                                                                  LGEATHSQTEVHLKTGGTVPPAAQQLHRENTQRTVQEALSASGVSPSDLSATATTTKPGL
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THRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNG
                                                   PPLHHAKNCDFSFTGLQHVTDKNNENRKQEEGIEKGQILSSAADIAATVQHTMACHLVKR
                                                                                                                              QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK
                                                                                                                                                                                                    ALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRLTNKVBFPFLVLLISGGHCLLALV
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Pred. No. 1.9e-
3; Mismatches
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08-NOV-2000;
15-NOV-2000;
                                              The invention describes isolated 38650, 28472, 5495, 65507, 81588 and 14354 nucleic acid molecules (I) and their encoded polypeptides (II). The 38650 nucleic acid molecule comprises a sequence encoding adenosine deaminase. The 28472 nucleic acid molecule comprises a sequence encoding a human glycoprotease. The 5495, 65507, 81588 and 14354 comprise sequences that encode a human seven transmembrane domain (7TM). The 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid and polypeptide sequences are useful for diagnosing, preventing or treating a subject with or at risk of developing a disorder, e.g. cancer or aberrant cellular proliferation and/or differentiation (e.g. breast, ovarian, prostate, colon or lung cancer), immune disorders, heart disorders, cardiovascular disorders, endothelial disorders, heartopoietic disorders, cardiovascular disorders, endothelial disorders, heart of disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               breast cancer; ovarian cancer; prostate cancer; colon cancer; lung cancer; immune disorder; heart disorder; cardiovascular disorder; endothelial disorder; hematopoietic disorder; blood vessel disorder; brain disorder; pain; metabolic disorder; liver disorder; diabetes; platelet disorder; carcinoma; sarcoma; leukaemia; Hodgkin's disease; autoimmune disorder; hypertension; atherosclerosis; heart failure; myocardial infarction; ischaemic heart disease; Crohn's disease; Grave's disease; Kawasaki syndrome; Raynaud's disease; aneurysm; cerebral ischaemia; peripheral neuropathy; Alzheimer's disease; enzyme.
                                                                                                                                                                                                                                                                                                                                       New adenosine deaminase, glycoprotease and seven transmembrane domain nucleic acids and polypeptides, designated 38650, 28472, 5495, 65507, 81588 and 14354, useful for treating e.g. leukemias, Hodgkin's disease
              blood vessel disorders, brain disorders, pain and metabolic disorders, liver disorders or platelet disorders. These disorders include carcino
                                                                                                                                                                                                                                                                                    Claim 4; Fig 8A-B; 178pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-029938/02.
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Matches 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; enzyme; cancer; aberrant cellular proliferation; differentiation; immune disorders; heart disorder; brain disorder; cardiovascular disorder; endothedial cell disorder; pain disorder; haematopoeitic disorder; blood vessel disorder; metabolic disorder; liver disorder; platelet disorder; glycoprotease.
                                                                                                               08-NOV-2000; 2000US-0246768P.
08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
                                                                                                                                                                                                                                                                                            09-JAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human glycoprotease encoded by cDNA 28472.
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  (LEIB/)
(KAPE/)
(GLUC/)
                                                                                                                                                                                                                           08-NOV-2001; 2001US-00012140
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LBIBY K R.
KAPELLER-LIBERMANN
GLUCKSMANN M A.
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The invention relates to an isolated 38650 (encoding adenosine CC deaminase), 28472 (encoding a Jycoprotease), 5495 (encoding a 7 CC transmembrane receptor), 65507, 81588 or 14354 nucleic acid molecule (or CC a sequence which is at least 60% identical to the six nucleic acids or CC naturally occurring variants, or a DNA insert of the plasmid deposited CC with the American Type Culture Collection as Accession No. not defined in CC the specification, which encodes the amino acid sequence). Also included CC are a host cell containing the nucleic acids (used to produce the CC proteins), the encoded proteins, an antibody that selectively binds to CC the polypeptide, and identifying a compound that binds to/modulates the activity of the polypeptide. The nucleic acid molecules, polypeptides and CC methods are useful for diagnosing, treating cancer, aberrant cellular CC proliferation and/or differentiation, immune disorders, heart disorders, CC cardiovascular disorders including endothelial cell disorders, pain and metabolic disorders are given in the specification). The present CC examples of these disorders are given in the specification). The present
  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated 38650, 28472, 5495, 65507, 81588 and 14354 nucleic molecules, useful for diagnosing, treating cancer, pain, or immu heart, endothelial cell, hematopoeitic, blood vessel, brain, met
                                                                                                            sequence is the Human glycoprotease encoded by cDNA 28472
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98.3%;
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IMIAWNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMBI
                                                        THRAILFCKQRDLLPQNNAVLVASGGVASNPYIRRALBILTNATQCTLLCPPPRLCTDNG
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Matches 361
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Yamamoto :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 364
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24-JAN-2002; 2002US-0350435P.
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J, Isono Y, I
Yoshikawa T, (
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                                                                                                      PPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKR
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                                                                                                                                                               QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK 240
                                                                                                                                                                                                                          ALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRLTNKVBFPFLVLLISGGHCLLALV 180
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IMIA 364
                                                                                    PPLHHAKNCDFPFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKR
                           THRAILFCKQRDLLPQNNAVLVASGGVASNFCIRRALEILTNATQCTLLCPPPRLCTDNG
                                                                                                                                                                                                        ALSLGVGLSFSLQLVGQLKKPFIPIHIMEAHALTIRLTNKVEFPFLVLLISGGHCLLALV
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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Pred. No. 7.9e-186;
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                                                      The invention describes an isolated nucleic acid molecule (I) encoding a CC metalloprotease (WP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder, an CC ameriorating a medical condition, particularly an immune disorder, an CC amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like condition. The compositions and methods are also useful for diagnosing, prognosticating, treating, ameliorating and/or treating disorders (C associated with MP-1 activity, e.g. diabetes, cancer, reproductive CC disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell aplasia), metabolic disorders (e.g. premature puberty, Kalman syndrome, CC or Cushing's syndrome), neurodegenerative disease (Alzheimer's disease, CParkinson's disease, Huntington's disease or Tourette syndrome), liver and renal disease, Huntington's disease or Tourette syndrome), liver and renal diseases, pulmonary diseases (e.g. puenmonia, emphysema or cystic (fibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This is the amino acid CC sequence of a metalloprotease MP1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and neurological disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5;
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10-APR-2001;
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 Query Match
                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                    Sequence 409 AA;
                                                                                                                                                                         New isolated nucleic acid genes from Drosophila and
                                                                                                                                              Disclosure; SEQ ID NO 34191; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 34191.
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11-JUL-2000; 2000US-00614150
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Best Local Similarity Matches 156; Conserv
09-MAR-1999
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  25-FEB-1999;
05-MAR-1999;
                                           25-FEB-2000;
                                                                     06-SEP-2000
                                                                                               EP1033405-A2
                                                                                                                       Arabidopsis thaliana.
                                                                                                                                                          protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 21029.
                                                                                                                                                                                                                                                         AAG19285;
                                                                                                                                                                                                                                                                                  AAG19285 standard; protein; 444 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         QILSSA-----ADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVA
                                                                                                                                                                                                                                                                                                                                                                               KCP 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --RSGGPAVEELALEGDAKSVKFNVPMKYHKDCNFSYAGLKTQVRLAIEAKE----IDAK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEQELSPPFMALLISGGHNLLVLAHKLGQYTQLGTTVDDAIGEAFDKTAKWLGLDMH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRL
                                                                                                                                                                                                                                                                                                                                                                                                     SNKYVRLRLNNI VENKULKLVCPPPSLCTDNGVMVAWTGLEHFRVG------
                                                                                                                                                 sequence.
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ilarity 40.8%;
Conservative 5
                                           200089-00101439
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                                            AAY52216;
                                                                                         AAY52216 standard;
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                                                                                                                                                                                                                                                                                                                                                                                        --RSGGPAVEELALEGDAKSVKFNVFMKYHKDCNFSYAGLKTQVRLAIEAKE----IDAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKG
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(first entry)
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99US-0159295P

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99US-0160768P

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99US-0160814P

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                                                                                         protein; 463
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40.8%; Pre
----ive 57;
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Pred. No. 3.3e-60;
7; Mismatches 127;
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                                                                                                                                                                                                                                                                                                    the ygjD family, after the name given to the Escherichia coli family member. These proteins are essential for the survival of both Gram negative and Gram positive bacteria, although no function has as yet been ascribed to these proteins. The ygjD proteins, fragments of ygjD proteins (for example, fragments encompassing one or more conserved ygjD motifs such as AAY52218-Y5284) and nucleotides encoding them can be used to identify antagonists and broad spectrum antibacterial compounds. These antagonists and compounds can be used to treat a wide range of bacterial infections. New antibiotics are urgently needed, as serious bacterial infections and antibiotic resistant strains are becoming increasingly prevalent. The proteins of the invention are essential proteins for bacterial viability, and represent new targets for antibiotics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel bacterial polypeptides used to identify broad spectrum antibiotics.
                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana ygjD protein homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteins AAY52202-Y52217 encompass a novel family of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLAX ) GLAXO GROUP LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ygjD protein; essential; Gram positive; Gram negative; conserved; motif; identification; antagonist; antibacterial; antibiotic; broad spectrum;
                           217
                                                                                                             142
                                                                                 158
                                                                                                                                                                                                                            145;
                                                                                                                                                                                              38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Fig 1; 55pp; English
                                                                                                                                                                                                                                         Similarity
                                                                                                          T-NKVEFPFLVILISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPEC
                                                                                                                                                                 463 AA
-- RSGGPAVEELALEGDAKSVKFNVPMKYHKDCNPSYAGLKTQVRLAIBAKE
                        STMSCGKALEHLAKQCKREHEDIKFFLHHAKKCUFSFTGLÚHVTDKI IMKKBKBEGIBKG
                                                     VEQELS PPFMALL I SGGHNLLVLAHKLGQYTQLGTTVDDA I GEAFDKTAKWLGLDMH----
                                                                                                                                                                                             IVLGIETSCDDTAAAVVDETGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQE
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Edgerton MD,
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152. .198
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208. .259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "ygjD conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .131
                                                                                                                                                                                                                                         29.8%;
37.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        resistance; drug target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "ygjD conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loferer H,
                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                         Score 634; DB 3;
Pred. No. 1.8e-57;
1; Mismatches 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peitsch MC
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                                                         aberrant glutamate transport or motor neuron disorder, such as amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like condition. The compositions and methods are also useful for diagnosing, prognosticating, treating, ameliorating and/or treating disorders associated with MP-1 activity, e.g. diabetes, cancer, reproductive disorders (e.g. Kleinfelter's syndrome, genital watts, or germinal cell aplasia), metabolic disorders (e.g. promature puberty, Kallman syndrome, parkings's syndrome, juverantive diseases (Alzheimer's disease, Parkinson's disease, Huntington's disease or Tourette syndrome), liver and renal diseases and immune disorders (e.g. AIDS, rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes an isolated nucleic acid molecule (I) encoding metalloprotease (MP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-FEB-2001; 2001US-0266518P.
10-APR-2001; 2001US-0282814P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; immuned disorder; rheumatoid arthritis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia; emphysema; cystic fibrosis; vascular disorder; inflammatory disorder; neurological disorder.
                                       or sepsis),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 50; 473pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-723329/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-FEB-2002; 2002WO-US003353.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG96489 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feder J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- IRNRADIAASFORVAVLHLEEKCERAIDWALE---LEPSIKHMVISGGVASNKYVRLR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----PKCPLGVDISKEVGEA 403
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                                pulmonary diseases (e.g. pneumonia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
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                                          emphysema or cystic
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RESULT 14
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PR 25-0
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Best Local (
                  the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for
                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-PEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bordetella
  proliferation;
                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                      Claim 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #8461.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU22934 standard; protein; 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELITRA PHARM
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Trawick
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                                                                                                                                                                                                                                                                                                                SEQ ID NO 50858; 1766pp; English.
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identifying a compound that
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Carr G
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Pred. No. 3.8e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haselbeck R, Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen
Forsyth
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  influences the
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Xu HH;
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  activity of
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cc the gene product or that has an activity against a biological pathway cc required for proliferation, or that inhibits cellular proliferation; (8) cc identifying a gene required for cellular proliferation or the biological cc pathway in which a proliferation required gene or its gene product lies cc or a gene on which the test compound that inhibits proliferation of an cc compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent co which each of the strains is present in a culture or collection of cc strains; or (13) identifying the target of a compound that inhibits the cc proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational cc drug discovery programs, or for screening homologous nucleic acids crequired for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target provbaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained cc fravior, int/nnh/nnh/liched for screening care.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                             84 QQLHRENIQRIVQEALSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFI 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
VVAGGVGANALLRAHLARALKPLRAEAYFPPLSLCTDNGAMIAFAAAERVKAGLADLRE 363
                                                                                                                    KIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVL
                                                                                                                                                                                                                                                               GIHHLEGHLLSPLLAEPRPEFPFVALLVSGGHTQLMLVDGVGRYELLGETLDDAAGEAFD
                                                                                                                                                                                                                                                                                                        PIHHMEAHALTIRLTN-KVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLD
                                                                                                                                                                                                                                                                                                                                                    SRDHIRRVVPLTRQVLAEAGLTLADVGAVAYTAGPGLAGALLVGASVAQALAWSRALPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                    HPGPRTLVVNSAPMIILGPESSCDETGVAAVCTERGLLAHALHTQIAMHQEYGGVVPELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPG--TLFLHK---IVLGIETSCDDTAAAVVDETGNVLGEAIHSQTEVHLKTGGIVPPAA
                                                                                  RV--KAATRDGGELGE--QDRADLAAATQAAIVEVLAAKAIRAL---KOTGL-----RRL
                                                                                                                                                                           KSAKLMGL-GYP-----GGPALARLAEQGDASRYDLPRPMLHSGDLDFSFSGLKTAVLT
                                                                                                                                                                                                                  KVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQ-HVTD
                                      VASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.7%; Score 524; DB 6; 37.3%; Pred. No. 5.7e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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ABG96491;
                   ABG96491 standard;
                   protein;
                    421
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Novel human metalloprotease associated protein

11-DEC-2002

(first entry)

RESULT 15
ABG96491
ID ABG96
XX motor neuron disorder; manyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Allman syndrome; Cushing's disease; Huntington's disease; Tourette syndrome; sepsis; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; immune disorder; rheumatoid arthritis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia; emphysema; cystic fibrosis; vascular disorder; inflammatory disorder; neurological disorder. Metalloprotease; MP-1; immune disorder; glutamate transport; cancer;

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The invention describes an isolated nucleic acid molecule (I) encoding a metalloprotease (MP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder, an aberrant glutemate transport or motor neuron disorder, such as amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like condition. The compositions and methods are also useful for diagnosing, prognosticating, treating, ameliorating and/or treating disorders group cassociated with MP-1 activity, e.g. diabetes, cancer, reproductive disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell aplasia), metabolic disorders (e.g. premature puberty, Kallman syndrome, or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, Parkinson's disease and immune disorders (e.g. AIDS, rheumatoid arthritis or sepsis), pulmonary diseases (e.g. memonia, emphysema or cystic fibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This is the amino acid sequence of a metalloprotease MP1 associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200272751-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 465-466; 473pp; English.
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10-APR-2001; 2001US-0282814P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
   389
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                                                                                                                                                                                                                                                                                                                                                                                                             218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J, Feder J, Nelson TC, Duclos
                                                                                                                                                                                                                                                                            275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 VLGIETSCDDTAAAVVDETGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQEA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 LSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRLT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
                                                              GAISKLSAAHNVTTIKVLLSLCTDNAEMIAYSGL-----LMLVNRSEAIWRRENDIPDT 367
                                                                                                                                                                                                                                                                                                                                        GIHVGAAVEILASRASADGHLRYPIFLPNVPKANMNFDQIKGSYLNLLERLRKNSETSID
-----KCPLGVDISKEVGEASIKVPQLKM 412
                                                                                                                      RALBILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYBP----- 388
                                                                                                                                                                                                                                                                                                                                                                                                          TMSGGKAIEHLAKQGN----RFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIE 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNDAGTSPKDLDAVAVTVTPGLVIALKEGISAAIGFAKKHRLFLIPVHHMRAHALSILLV 144
                                                                                                                                                                                                      -----IPDFCASLONTVARHISSKLHIFFESLSEQEKLPKQ---LVIGGGVAANQVIF 313
                                                                                                                                                                                                                                                                  KGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIR 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLGIETSCODTAVAI VNEKREILSSERYTERAI QRQQGGINPSVCALQHRENLPRLIEKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.7%; Score 524; DB 5; Length 421; 33.4%; Pred. No. 6.7e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77; Mismatches 146; Indels
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> 밁 368 IYAHARSDIGTDASSEI----IDTPRRKL 392

Search completed: February 16, 2005, 13:05:54 Job time: 91.25 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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US-10-67-443-2
; Sequence 2, Application US/10067443
; Patent No. 6642041
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	5019, Ap	6933, Ap	3197, Ap	5050, Ap	13545, A	6, Appli	6, Appli	5, Appli	5, Appli	12013, A	144, App	33046, A	4387, Ap	19489, A	728, App	6, Appli	4609, Ap	

### ALIGNMENTS

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301	241	181 181	121	61	д д	2 2	437 "9666999 HZ
						ch ll Simi: 414;	L INFORMATION: LANT: BRISTOL-MYSER SQUID OP INVENTION: POLYNUCLEO OP INVENTION: SPINAL CO REFERENCE: D0073 NP NT APPLICATION NUMBER: US A
AILPC	HAKO HAKO	SDFLL		AIHSQ 	LIKIA LIKIA	larit Conse	TION: Stol- TION: TION: TION: TION: TOO: DOO: DOO: DATE: ION NATE: ATE: NTON NATE: NTON NATE: ATE: ATE: ATE: ATE: ATE: ATE: ATE:
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ASGG	TIMO TIMO	KVARI	IPIH HIPIH	A — A — A — A — A — A — A — A — A — A —	LRSFI       LRSFI	Score 212 Pred. No. Mismatc	L INFORMATION:  LANT: Bristol-Myers Squibb Company OP INVENTION: POLYNUCLEOTIDE ENCODI OP INVENTION: POLYNUCLEOTIDE ENCODI OP INVENTION: SPINAL CORD, MP-1 EXPERENCE: DO073 NP ST PILING DATE: 2002-02-05 APPLICATION NUMBER: US 60/266,518 FILING DATE: 2001-02-05 APPLICATION NUMBER: US 60/282,814 FILING DATE: 2001-04-10 APPLICATION NUMBER: US 60/282,814 RILING DATE: 2001-04-10 APPLICATION PRICE CONTROL OF SEQ ID NOS: 71 ARE: PATENTING DATE: 2001-04-10 RILING DAT
ASNP             ASNP		1757       1757	MBAH MBAH		NEH PG	ore 2125; ced. No. 1. Mismatches	ny CODIN 1 1 18 18
YIRRA       YIRRA	GIBKC	KHPEC	ALTI 	QRIVO	TLFLI 	4	G >
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HATO	SAADI       SAADI	GEKAI	VEPPF 	ASGVS           ASGVS	GIETS	Length Indels	META
	AATV	EHILA:	TATT7	PSDLS       PSDLS		th 414;	LOPRO
	AMIH           AMIH	QCNRI COGNRI	SGGH	TAIAT	AAVVI	0;	)TEAS
THRAILECKORDLLEVINAVIVASGGVASNEYIRRALEILTNATOCTILLCEPERLCTING	PPLHHAKNCDPSPTGLQHVTDKI IMKKEKEBGI BKGQI LSSAADI AATVQHTMACHLVKR 	QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK 	ALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRLTNKVBFPFLVILISGGHCLLALV 	LGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQEALSASGVSPSDLSAIATTIKPGL 	MLILTKTAGVEFKPSKRKVYBELRSFNFHPGTLFLHKIVLGIETSCDDTAAAVVDETGNV 	Gaps	FORMATION:  'Bristol-Myers Squibb Company INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED INVENTION: SPINAL CORD, MP-1 INVENTION: SPINAL CORD, MP-1 PARICE: D0073 NP PAPELICATION NUMBER: US/10/067,443  'ILING DATE: 2002-02-05 'ILICATION NUMBER: US 60/266,518 LICATION NUMBER: US 60/266,518 LICATION NUMBER: US 60/282,814 LICATION NUMBER: US 60/282,814  LICATION NUMBER: US 60/282,814  ING DATE: 2001-04-10  'SEQ ID NOS: 71  PatentIn version 3.0  2 414 414 T. Homo sapiens
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; Sequence 22, Application US/10067443
; Patent No. 6642041
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/067,443;
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 19
                                                                                                                 US-10-067-443-22
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-067-443-19
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PATENT NO. 6642041
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: DOO73 NP
FILE REFERENCE: DOO73 NP
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Best Local Similarity 93.8
Matches 412; Conservative
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CURRENT APPLICATION NUMBER: US/10/067,443;
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 22
LENGTH: 267
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; ORGANISM: homo
US-10-067-443-22
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                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3 Patent No.
                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED IN
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
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                                                                                                                                                                                                                                                                              LENGTH: 463
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                                                                                                                          cch 29.8%; Score 634; DB 4; Length 463; al Similarity 37.9%; Pred. No. 1.8e-63; 1.45; Conservative 61; Mismatches 129; Indels 48;
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267; Conserv
                                                                        38 IVLGIETSCDDTAAAVVDETGNVLGBAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQE
ALSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRL 157
                                           VVLGIETSCDDTAAAVVSPFNHLSSSC---RAELLVQYGGVAPKQAEEAHSRVIDKVVQD 141
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Gaps

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PATENT NO. 6642041

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: North Polynucleotide encoding a 1
TITLE OF INVENTION: SPINAL CORD, MP-1
TITLE OF INVENTION: SPINAL CORD, MP-1
PILB REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-067-443-25
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                GENERAL INFORMATION:

APPLICANT: Bristol-Myere Squibb Company

TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED

TITLE OF INVENTION: SPINAL CORD, MP-1
                                                                                                                   Sequence 4, Application US/10067443 Patent No. 6642041
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PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
       FILE REFERENCE: D0073 NP
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Pred. No. 2e-54;
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PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 4
LENGTH: 421
TYPE: PRT
ORGANISM: Caenorhabditis elegans
                                                                                         ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-067-443-28
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US-10-067-443-28
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                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: BRISTOL MYERS SQUIDD COMPANY
TITLE OF INVENTION: FOLYNUCLECTIDE ENCODING
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: DO073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
Query Match 24.7%; Score 524; DB 4; I Best Local Similarity 33.4%; Pred. No. 6.3e-51; Matches 130; Conservative 77; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description US/10067443
Patent No. 6642041
                                                                                                                                                                                     SEQ ID NO 28
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Best Local Similarity
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                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOPTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/266,518 PRIOR FILING DATE: 2001-02-05
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CURRENT FILING DATE: 2002-02-05
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                                                                                                                                                             LENGTH: 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNDAGTSPKDLDAVAVTVTPGLVIALKEGISAAIGFAKKHRLPLIPVHHMRAHALSILLV 144
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US-09-540-236-2726
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APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT APPLICATION NUMBER: US/09/540,236
NUMBER OF SEQ ID NOS: 3840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2726
LENGTH: 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                                                                          FNEMLDQANITKSDIDAVAYTKGPGLIGALMTGALFGRTLAYGLGVPAVGVHHMEGHLLA 125
                                                                                                                                                                                                                                                                                                         VIGLETSCDETGLAIYDSTMNGRGGVLSQVLYSQINLHATYGGVVPELASRDHIRKLVPL
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   IRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAG---
                                                                  IEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFY 332
                                                                                                                                                                                                                                                                         VQEALSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALT 154
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                                    -ATRADIAASFEYAVVDTLVKKCTKALQMTGIRQ------LVVAGGVSANQT 284
                                                                                                     -GGPNIEKLAKNGNPHAYELPRPMQH-KGLDFSFSGMKTAIHNLIKDTPNAQS
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US-08-087-797-3
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US-09-252-991A-17372
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Matches
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LENGTH: 401
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                       Sequence 3, Applic
Patent No. 5543312
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                                                                                     GENERAL INFORMATION:
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APPLICANT: Mellors, Alan
APPLICANT: LO, Reggie Y.C.
APPLICANT: Abdullah, Khalid M.
TITLE OF INVENTION: Pasteurella H
TITLE OF INVENTION: Glycoprotease
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133; Conserv
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                                                                                                                      Application US/08087797
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                   Haemolytica
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Sequence 17372, Application US/09252991A Patent No. 6551795
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                          ---KOTGL--KN---LVIAGGVSANQALRSGLEKMLGEMKGQVFYARPRFCTDNGAMIAY
                                                                                                                                                              LFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAW 365
                                                                                                                                                                                                                           RPGLDFSFSGLKTFTLN-TWQRCVEAGDDSEQ---TRCDIALAFQTAVVETLLIKCRRAL
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AGCQRLLAG---QHDGPAISVQPRWPM
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34.4%; Pred. No. 3.8
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                      GENERAL INFORMATION:
APPLICANT: GARY BREYON
APPLICANT: GARY BREYON
TITLE OF INVENTION: MUCLEIC ACID AND ANIMO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
                                                                                                                                             Sequence 6513, Application US/09543681A Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 23.0%; Score 488; DB 1; Length 342; Best Local Similarity 35.4%; Pred. No. 6e-47; Matches 126; Conservative 51; Mismatches 155; Indels
CURRENT APPLICATION NUMBER: US/09/543,681A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Layton, Jr., Samuel G.
REGISTRATION NUMBER: 22807
REFERENCE/DOCKET NUMBER: 337
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1'CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: No. 5543312th Carolina
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                                                                                                                                                                                                                                                                                                                                                                                               ---TRADIARAFEDAVVDTLMIKCKRA-----
                                                                                                                                                                                                                                                                                                  LAEMMKKRRGEVFYARPEFCTDNGAMIAYAGMVRFKA--GATADL-GVSVRPRWPL
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SEQ ID NO 6513
LENGTH: 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
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                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                 APPLICATION NUMBER: US/08/087,797
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lo, Reggie Y.C.
APPLICANT: Abdullah, Khalid M.
TITLE OP INVENTION: Pasteurella Haemolytica
TITLE OP INVENTION: Glycoprotease
TITLE OP INVENTION: Gene and the Purified E
TELECOMMUNICATION INFORMATION: TELEPHONE: 704 377 1561
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                                 NAME: Layton, Jr., Samuel G.
REGISTRATION NUMBER: 22807
REFERENCE/DOCKET NUMBER: 337.
                                                                                                                                                                                                                                                                                                                                                                     CITY: Charlotte
STATE: No. 5543312th Carolina
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                                                                                                                                                                                                                                                                                                                                 ZIP: 28234
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                                                                                                                                                                                                                                                                                                                                                                                                                     1211 Bast Morehead Street,
                                                                                                                                                                                                                                                                                                                                                     United States
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FILE BEFERENCE: 2709.204001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 9221

LENGTH: 343

TYPE: PRT

ORGANISM: Xlebsiella pneumoniae
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                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
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LENGTH: 325 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 AEMMKKLKGEVFYPRPQFCTDNGAMIAYTGFLRLK 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 TNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120;
                                                                                                                                                                                                                                  123;
                                                                                                                 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 VLGIETSCDDTAAAVVDETGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQEA
                                                                                                                                                                                        39 VLGIETSCDDTAAAVVDETGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQEA 98
                                                                                                                                                       9
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                                   TNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECS 217
                                                                                                               LSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIFIHHMEAHALTIRL- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLR 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILSSAADIAATVOHTMACHLVKRTHRAILFCKORDLLPQNNAVLVASGGVASNFYIRRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---AGVAMSKLABSGTPNRFKFPRPMTDRPGLDFSFSGLKTFAANTIKANLNENGELDEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMBAHALTIRL- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILGIETSCDETGVAIYDEDKGLVANOLYSQIDMHADYGGVVPELASRDHIRKTLPLIQEA
DNPPAFPFVALLVSGGHTQLISVTGIGQYELLGESIDDAAGEAFDKTAKLLGL-DYP---
                                                                         LKEAGLTAKDIDAVAYTAGPGLVGALLVGATVGRALAPAWNVPAIPVHHVEGHLLAPMLE
                                                                                                                                                     VLGIETSCDETGIAIYDDQQGLLANQLYSQVKLHADYGGVVPELASRDHVRKTVPLIQAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---TKCDIAHAFQQAV------VDTILIKCK-RALEQTGYKRLVMAGGVSANKQLRADL
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.4%; Score 475.5;
35.8%; Pred. No. 1.5e
tive 47; Mismatches
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                                                                                                                                                                                                                                51;
                                                                                                                                                                                                                              Score 474.5; DB 4;
Pred. No. 2.1e-45;
51; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.5e-45;
                                                                                                                                                                                                                                                                  DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149;
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 325;
                                                                                                                                                                                                                                                                  Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                Gaps
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US-09-107-532A-6609
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                                                                                                                          US-09-107-532A-6609
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Patent No. 6583275
GENERAL INFORMATION:
                                                           Query Match
Best Local Similarity
                                             Matches
                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 6609: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                        NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...363
SEQUENCE DESCRIPTION: SEQ ID NO: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Ariniello, Pamela Deneke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                             119;
  37 KIVLGIETSCDDTAAAVVDETGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAEMMQKRGGEVFYARPEFCTDNGAMIAYAGMVRLQTGA----KAELGVTVRPRWPL
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OPERATING SYSTEM: <Unknown>
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                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 40,489
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                                                                                                                                                                                                                                                                                                                                            ENGTH: 363 amino acids
                                             Conservative
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                                                              22.2%;
35.7%;
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                                         Score 472; DB 4;
Pred. No. 4.5e-45;
9; Mismatches 123
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                                                                                                                                              6609:
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AND AMINO ACID SEQUENCES RELATING TO
FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                             123;
                                                                                Length 363;
                                             Indels
                                             32;
                                             Gaps
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                                                                                                                                         Query Match
Best Local Similarity
Matches 116; Conserv
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GENERAL INFORMATION:
APPLICANT: Hoskins, Jo Ann
APPLICANT: Tang, Joseph Chiou-Chu
APPLICANT: Treadway, Patti Jean
TITLE OF INVENTION: Streptococcus
TITLE OF INVENTION: Gcp
                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ,IBM PC compatible
COMPUTER: ,IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/987,121A
                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
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ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 333 IRRALEILTNA--TOCTLLCPPPRICTDNGIMI 363
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     64
                 97 EALSASGYSFSDLSAIATTIKFGLALSIGVGLSFSLQLVGQLKKPFIFIHAMBAHALTIR 156
                                                                                       89
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                                                                  4 RYILAPETSCDETSVAVLKNDDELLSNVIASQIESHKRPGGVVPEVASRHVEVITACIE 63
-SYPSGKEIDQLAHQGKDNYHF--PRAMIHEDNYDFSFSGLKSAFINLVHNAQQRGEDLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EALSASGVSPSDLSAIATTIKPGLALSIGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KN------DLAASFQASVIDVLITKTLRA---C-----QNYPVKQLVVAGGVAANQG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAV--LVASGGVASNFY 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indiana
                                                                                                                                     21.7%; Score 461; DB 3; Length 336; ilarity 34.5%; Pred. No. 7.3e-44; Conservative 58; Mismatches 132; Indels
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                                                                                                                                                                                                                                                                                                                                   317-276-3334
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                                                                                                                                         30;
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                                                                                                                                                                                                                           157 LTNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPEC 216
                                                                                                                                                                                                         124 SVEPLEFPLLALLVSGGHTELVYVSEAGDYKIVGETRDDAVGEAYDKVGRVMGL-----
                              LEILTNATQCTLLCPPPRLCTDNGIMIA-----WN 366
                                                       QILSSAADIAATVOHTMACHLVKRTHRAILFCKORDLLPONNAVLVASGGVASNFYIRRA 336
L--ATBITDVNVIIPPLRLCGDNAGMIAYASVSEWN 315
                                                                                                                                                                    STMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKG 276
                                                                                                                                     -TYPAGREIDELAHOGHDI-YDPPRAMIKEDNLEFSFSGLKSAFINLHHNAE-----QKG
                                                                                                                                     230
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Search completed: February 16, 2005, 13:10:24 Job time: 27.75 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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US-10-649-273-2
US-10-651-722-2
US-10-649-273-19
US-10-649-273-19
US-10-649-273-19
US-10-012-140-2
US-10-012-149-2039
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Sequence 67993, A	65768,		e 52054,	e 58204,			68438,	78161,	7548	e 56695,	_	e 55404,	æ		672	e 6319	24,	28,	4, 2	28,	4	N	0 4	50	e 25	e 25, App	e 25, App	e 25, App	Sequence 113732,	3, App	Sequence 3, Appli

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; ORGANISM: Homo sapiens
US-10-067-443-2
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TITLE OF INVENTION: POLYMUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: DO073 NP
FILE REFE
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Publication No. US20040043407A1
GENERRAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYMUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
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Best Local
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IMIAWNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI 414
                            THRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALBILTNATQCTLLCPPPRLCTDNG
                                            THRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNG
                                                                                   PPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKR
                                                                                                       PPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKR
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Sequence 2, Application US/10651722

Publication No. US20040043302A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722

CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2

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US-10-651-722-2
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Best Local Similarity 100.0%; Pred. No. 1:
Matches 414; Conservative 0; Mismatches
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
FULE REFERENCE: D0073 NP
CURRENT FAPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
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US-10-649-273-19
Sequence 19, Application US/10649273
Publication No. US20040043407A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A N
FILE REFERENCE: DO073 CNT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2002-05
PRIOR FILING DATE: 2002-05
PRIOR FILING DATE: 2001-04-10
NUMBER: OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 19
                                  ; TYPE: PRT ; ORGANISM: homo sapiens US-10-649-273-19
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PRIOR APPLICATION NUMBER: US 60/282,814
-PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
LENGTH: 439
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Best Local Similarity 93.8%;
 Query Match
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ORGANISM: homo sapiens
.10-067-443-19
                                                                                            LENGTH: 439
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 98.4%;
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 Score 2090.5;
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Length 439;
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                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.2 SEQ ID NO 19
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR PILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER: OS 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER: DECOLITOR US 10/067,814
                                                                                                                                                                                                                                                                                 LENGTH: 439
TYPE: PRT
ORGANISM: homo @
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 121 ALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRLTNKVEFPFLVLLISGGHCLLALV 180
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                                                                                                           1 MLILTKTAGVFFKPSKRKVYEFLRSFNFHPGTLFLHKIVLGIETSCDDTAAAVVDETGNV
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                                                     LGENINGCTTVILKTGGIVEFAAQQLHKENIQKIVQBALSASGVSPSDLSAIATTIKPGL 120
                                      LGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQEALSASGVSPSDLSAIATTIKPGL
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                                                                                                                                                                                    Score 2090.5; DB Pred. No. 4e-196; 0; Mismatches
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Sequence 5, Application US/10012140

Publication No. US20030009017A1

GENERAL INFORMATION:
APPLICANT: Leiby, Kevin R.
APPLICANT: Leiby, Kevin R.
APPLICANT: Glucksmann, Maria A.
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 381552004900
CURRENT APPLICATION NUMBER: US/10/012,140
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 60/246,768
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-108
PRIOR FILING DATE: 2000-11-108
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PRIOR FILING DATE: 2000-11-15
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 414
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Best Local :
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nes 407; Conserv
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PPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKR 300
                                                      QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGMRFHFDIK 240
                                                                                                                              ALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRLTNKVBFPFLVLLISGGHCLLALV 180
                                                                                                                                                                            LGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQEALSASGVSPSDLSAIATTIKPGL
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                                                                                                                                                                                                                                                                                                                     98.3%; Score 2088; DB 14; Length 414; 98.3%; Pred. No. 6.4e-196; ative 3; Mismatches 4; Indels 0
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NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2039
LENGTH: 364
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-094-749-2039
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APPLICANT: MASCHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: U007-03-12
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
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                                                                                                                                                                                                                                                                                                                                                                                          Matches 361; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: JP 2001-328381 PRIOR FILING DATE: 2001-09-14
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SUGIYAMA,
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PPLHHAKNCDFSFTGLQHVTDKI IMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKR
                                                             QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK 240
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
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YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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SATO, HIROYUKI
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YAMAMOTO, JUN-ICHI
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99.2%;
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Pred. No. 3.8e-172;
n: Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 364;
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                                                                                                                                                                                             Sequence 22, Application US/10649273
Publication No. US20040043407A1
GENERAL INFORMATION:
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         APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 CNT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/262,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILLING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
NUMBER OF SEQ ID NOS: 71
NUMBER OF SEQ ID NOS: 71
PRIOR FILING DATE: 2002-02-05
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-649-273-22
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US-10-651-722-22
                                                                                                                                                                                                                                                                                                                                            US-10-651-722-22
                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 22
LENGTH: 267
TYPB: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/10651722
Publication No. US20040048302A1
GENERAL INFORMATION:
APPLICANT: Briscol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
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PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
                                                                                                                                                                                                                                                                            Local Similarity
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268 EKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGV 327
                                                                                          208 LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKK 267
                                                                                                                                                                                    148 MEAHALTIRLTNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR 207
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Similarity 100.0%;
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                                                                     LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKK
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                                                                                                                                                                                                                                                                     65.2%; Score 1385; DB 15; 100.0%; Pred. No. 3.5e-127;
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US-10-424-599-209259
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US-10-424-599-209259
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Sequence 3, Application US/10067443
Publication No. US20030082782A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (532218)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 209259
TENCTH. AAC
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ORGANISM: Glycine max
FEATURE:
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Similarity 43.1%; Pred. No. 8.8e-58;
55; Conservative 54; Mismatches 126; Indels 25;
                                                                                                                                                                                                                                                                                                                YIRRALBILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYBPKCP 391
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                                                                           A NOVEL METALOPROTEASE HIGHLY EXPRESSED
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A N
FILE REFERENCE: D0073 CWT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PALENTIN VETSION 3.2
SEQ ID NO 3
                                                                                            ; ORGANISM: Arabidopsis thaliana 
US-10-649-273-3
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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-067-443-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-649-273-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/10649273 Publication No. US20040043407A1 GENERAL INFORMATION:
Query Match 29.8%; Score 634; DB 15; Best Local Similarity 37.9%; Pred. No. 4.3e-53; Matches 145; Conservative 61; Mismatches 129
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PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bristol-Myers Squibb Company
                                                                                                                                        TYPE: PRT
                                                                                                                                                        ENGTH:
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; TYAPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-651-722-3
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CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOPTWARE: PatentIn version 3.2
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Publication No. US20040048302A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            Query Match 29.8%; Score 634; DB 15; Length 463; Best Local Similarity 37.9%; Pred. No. 4.3e-53; Matches 145; Conservative 61; Mismatches 129; Indels 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
                                            217
                                                                                                                                                                              142 ALDKANLTEKDLSAVAVTIGPGLSLCLRVGVRKARRVAGNFSLPIVGVHHMEAHALVARL
259 -- RSGGPÄVEBLALEGDAKSVKFNVPMKYHKDCNFSYAGLKTQVRLAIBAKB------
                                                                                    202 VEQELSPPFMALLISGGHNLLVLAHKLGQYTQLGTTVDDAIGEAPDKTAKWLGLDMH--- 258
                                                                                                              158 T-NKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPEC 216
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                                                                                                                                                                                                                                                                     85 VVLGIBTSCDDTAAAVVSPFNHLSSSC---RAELLVQYGGVAPKQABBAHSRVIDKVVQD
                                                                                                                                                                                                                                                                                               85 VVLGIETSCDDTAAAVVSPFNHLSSSC---RAELLVQYGGVAPKQAEEAHSRVIDKVVQD 141
                                        STMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKG 276
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414 DYVYDLRPRWPLGEEYAKGRSEA 436 309 -- IRNRADIAASFQRVAVLHLEEKCERAIDWALE---LEPSIKHMVISGGVASNKYVRLR 363 LNNIVENKNLKLVCPPPSLCTDNGVMVAWTGLEHFRVG-----RYDPPPPATEPE 413 LEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYE----------PKCPLGVDISKEVGEA 403

Search completed: February 16, 2005, 13:28:29 Job time : 242.85 secs

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Title:
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Pending Patents AA Main:*

1: /cgn2_6/ptodata/1/paa/PCTUS COMB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1 PCT-US02-03 Sequence GENERAL 1 APPLICAN TITLE OF FILE REF CURRENT CURRENT PRIOR AF P		4.4 5	43	41	40	38	36 37	35	. u. u 4	32	30	29	27	25 26	24	22	21	20	18	16	14	13	121	10	۵ م	7	o 0	.4.	ω N F	. !	Result
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03353-2  (Ref. Application PC, INFORMATION: ANT: Bristol-Myers OF INVENTION: POLYN EFFERENCE: DO073 PCT TR APPLICATION NUMBER: TFILING DATE: 2001 APPLICATION NUMBER: FILING DATE: 2001-0 APPLICATION NOS: 71 EE: PatcmtIn versio NO 2 H: 414 PRT ISM: Homo sapiens		29.8 29.8	9 !	۰.		. 20	 	ω.	ພຸພ	. α	۰.5	ູ ທຸ	ייי		5	ກຸຕ	5 .	л ·		٠,6	ω.	. 8		8	100.0				100.0	> į	Query Match
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2-03353-2 2-03353-2 2-03353-2 3L INFORMATION: LINFORMATION: CANT: Bristol-Myers Squibb Company 3 OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL REFERENCE: D0073 PCT REFERENCE: D0073 PCT NOT APPLICATION NUMBER: PCT/US02/0353 NOT FILING DATE: 2002-02-05 APPLICATION NUMBER: US 60/266,518 FILING DATE: 2001-02-05 APPLICATION NUMBER: US 60/282,814 FILING DATE: 2001-04-10 R OF SEQ ID NOS: 71 3.00 3.00 3.00 3.00 3.00 3.00 3.00 3.0	ALIGNMENTS	US-10-649-273-3 US-10-651-722-3	US-09-708-427-16627	-10-449-902-4898 -11902-03353-3	US-09-513-996A-21029	US-10-424-599-209259	US-60-191-637-33775 US-60-191-681-26629	US-09-614-150A-34191	US-60-173-464-26192	US-60-243-748-1011 US-60-243-742-177	US-60-495-114-1373	US-60-262-814-22	US-10-918-754-1373	US-10-649-273-22 US-10-651-722-22	PCT-US02-03353-22	US-60-495-114-1374	US-10-918-754-1375	US-60-495-114-1371	US-10-1/0-2055-2/31/ US-10-918-754-1371	US-10-094-749-2039	US-60-282-814-19 US-10-012-140-5	US-60-266-518-19	US-10-649-273-19 US-10-651-722-19	PCT-US02-03353-19	US-10-918-754-1372	US-60-282-814-2	US-10-651-722-2	US-10-649-273-2	PCT-US0Z-03353-Z PCT-US0Z-19360-8 US-10-480-988-8	TOO 0000	ID
METALOPROTEASE, MP-1		Sequence 3, Appli Sequence 3, Appli	ce 16627,	48987,	Sequence 21030, A	20	26	44	261	17	1 4	22	Sequence 1373, Ap	222	20 5	Ξü,	Ti t	Sequence 1371, Ap	13,	20.	5 19	19	19	9	<u>.</u> ۳	2	Sequence 2, Appli	, 2	m ·		Description

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; Sequence 8, Application PC/TUS0219360
GENERAL INFORMATION:
GENOMICS, INC.
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: GANDHI, Ameena R.
APPLICANT: KABLE, Amy E.
APPLICANT: SWARNAKAR, Anita
APPLICANT: HAPALIA, April J.A.
APPLICANT: TRAN, Bao
APPLICANT: DUGGAN, Brendan M.
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                                                                               YAO, Monique G.
WALIA, Narinder K.
WASON, Patricia M.
GURURAJAN, Rajagopal
                                                                                                                                                                                                                                                                                                                                                                                DUGGAN, Brendan M. WARREN, Bridget A. ISON, Craig H. HONCHELL, Cynthia D. NGUYEN, Danniel B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK 240
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                    BECHA, Shanya I
LEE, Soo Yeun
TRAN, Uyen K.
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   TRAN, Uyen K.
ELLIOTT, Vicki S
                                                  LEE, Sally
BECHA, Shanya D.
                                                                                                                                                 BAUGHN, Mariah R. BOROWSKY, Mark L.
                                                                                                                                                                                                                  YANG, Junming
THANGAVELU, Ka
                                                                                                                                                                                                                                                                   RAMKUMAR, Jayalaxmi
GRIFFIN, Jennifer A.
                                                                                                                                                                                                                                                                                                   FORSYTHE, Ian
BARROSO, Ines
                                                                                                                                                                                                    GIETZEN, Kimberly J
                                                                                                                                                                                                                                                    LI, Joana X.
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E, Ernestine A.
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                                                                                                                                                                                                                                                                                                                   Ian J.
                                                                                                                                                                                                                     Kavitha
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PRIOR PILING DATE: 2001-06-22
PRIOR PILING DATE: 2001-06-06
PRIOR PILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US 60/303,445
PRIOR APPLICATION NUMBER: US 60/305,405
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: US 60/311,442
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-08-29
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PRIOR PILING DATE: 2001-08-29
PRIOR PILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PERL PROGRAMMER: US 60/378,205
PRIOR PILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PERL PROGRAMMER: US 60/378,205
PRIOR PILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PERL PROGRAMMER: US 60/378,205
PRIOR PILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 56
RESULT 3
US-10-480-988-8
; Sequence 8, Application US/10480988
; GENERAL INFORMATION:
; APPLICANT: GANDHI, Ameena R.; KABLE, Am
; APPLICANT: SWARNAKAR, Anita; HAFALIA,
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Best Local (
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FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7632424CD1
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                      Amy
     April J.A.;
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APPLICANT: LUO, Wen
APPLICANT: SPRAGUE, William
APPLICANT: TANG, Y. Tom
APPLICANT: LU, Yan
APPLICANT: LU, Yan
APPLICANT: ZEBARJADIAN, Yeganeh
APPLICANT: ZEBARJADIAN, Yeganeh
TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES
FILE REFERENCE: PF-1040 PCT
CURRENT APPLICATION NUMBER: PCT/US02/19360
CURRENT FILING DATE: 2002-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 100.0%; Score 2125; DB 1; Length Local Similarity 100.0%; Pred. No. 1.2e-214; nes 414; Conservative 0; Mismatches 0; Indels
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IMIAWNGIERLRAGIGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI
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APPLICANT: YUÉ, Henry; FORSYTHE, Ian J.;
APPLICANT: BARROSO, Ines; RAMKUMAR, Jayalaxmi;
APPLICANT: BARROSO, Ines; RAMKUMAR, Jayalaxmi;
APPLICANT: BARROSO, Jensifer A.; LI, Joana X.;
APPLICANT: YANG, Junming; THANGAVELU, Kavitha;
APPLICANT: BAUGHN, Mariah R.; BOROWSKY, Mark L.;
APPLICANT: YAO, Monique G.; CHAWLA, Narinder K.;
APPLICANT: YAO, Monique G.; CHAWLA, Narinder K.;
APPLICANT: LEE, Sally; BECHA, Ghanya D.;
APPLICANT: LEE, Sally; BECHA, Shanya D.;
APPLICANT: LEE, Soo Yeun; TRAN, Uyen K.;
APPLICANT: EE, Soo Yeun; TRAN, Uyen K.;
APPLICANT: BILIOTT, Vicki S.; LUO, Wen;
APPLICANT: BILIOTT, VICKI S.; LUO, Wen;
APPLICANT: LU, Yan; ZEBAROJADIAN, Yeganeh
TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES
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US-10-480-988-8
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CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: PCT/US02/19360
PRIOR FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/300,508
PRIOR APPLICATION NUMBER: US 60/303,445
PRIOR APPLICATION NUMBER: US 60/303,445
PRIOR FILING DATE: 2001-07-06
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US 60/305,405
PRIOR APPLICATION NUMBER: US 60/305,405
PRIOR APPLICATION NUMBER: US 60/305,405
PRIOR APPLICATION NUMBER: US 60/311,442
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SOFTWARE: PERL Program
SEQ ID NO 8
LENGTH: 414
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NAME/KEY: misc_feature
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THRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNG 360
                                          PPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKR 300
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; ORGANISM: Homo s
US-10-649-273-2
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: FOLYNUCLEOTIDE ENCODING A I
FILE REFERENCE: D0073 CNT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
RESULT 5
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US-10-649-273-2
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PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
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Sequence 2, Application US/10651722
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29

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Sequence 2, Application US/60266518
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITILE OF INVENTION: POLYNUCLECTIDE ENCODING A:
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCB: D0073 PSP:
CURRENT APPLICATION UNMBER: US/60/266,518
CURRENT FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 28
SOPTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 414
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PRIOR FILING DATE: 2001-02-05
PRIOR PPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 2
LENGTH: 414
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; ORGANISM: Homo
US-60-266-518-2
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US-60-266-518-2
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; ORGANISM: Homo
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                                                                               Score 2125; DB 37;
Pred. No. 1.2e-214;
; Mismatches 0;
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Pred. No. 1.2e-214;
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(GREERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A 1
TITLE OF INVENTION: SPINAL CORD, MF-1
FILE REFERENCE: DOOJS SEPI
CURRENT APPLICATION NUMBER: US/60/282,814
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 2125; DB 37; Best Local Similarity 100.0%; Pred. No. 1.2e-214; Matches 414; Conservative 0; Mismatches 0;
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TYPE: PRT
ORGANISM: Homo
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CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOPTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 1372
LENGTH: 425
TYPE: PRT
ORGANISM: Homo sapiens
US-60-495-114-1372
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Sequence 1372, Application US/10918754
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC
TITLE OF INVENTION: ENCODING HUMAN PROTEASE
TITLE OF INVENTION: USES THEREOF
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US-60-495-114-1372
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US-10-918-754-1372
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CURRENT FILING DATE: 2004-08-16
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1372
LENGTH: 425
                                                                                                                                                                                                                                                                                     Sequence 1372, Application US/60495114 GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                             APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001480
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PROTEINS, METHODS OF DETECTION
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RESULT 10

PCT-US02-03353-19

FCT-US02-03353-19

FSequence 19, Application PC/TUS0203353

FGENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A PRICE REFERENCE: D0073 PCT

CURRENT APPLICATION NUMBER: PCT/US02/03353

CURRENT FILING DATE: 2002-02-05

CURRENT FILING DATE: 2002-02-05
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Best Local Similarity
Matches 414; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 19
                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOPTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/266,518 PRIOR FILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: homo
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                                                 121 ALSLGVGLSFSLQLVGQLKKPPIPIHHMEAHALTIRLTNKVEFPPLVLLISGGHCLLALV 180
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Pred. No. 6e-211;
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US-10-649-273-19
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Best Local Similarity 93.8%;
Matches 412; Conservative
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PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 CNT
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CURRENT FILING DATE: 2003-08-27
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; Sequence 19, Application US/60266518
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
; TITLE OF INVENTION: SPINAL CORD, MP-1
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US-10-651-722-19
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE,
FILE REPERENCE: D0073 DIV
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Best Local Similarity 93.8%;
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PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
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CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2002-02-05
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; FILE REFERENCE: D0073 PSP; CURRENT APPLICATION NUMBER: US/60/; CURRENT FILING DATE: 2001-02-05; NUMBER OF SEQ ID NOS: 28; SOFTWARE: Patentin version 3.0; SEQ ID NO 19; LENGTH: 439; TYPE: PRT; ORGANISM: homo sapiens
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US-60-282-814-19
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: DO073 PSP1
CURRENT APPLICATION NUMBER: US/60/282,814
CURRENT APPLICATION NUMBER: US/60/282,814
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.0
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Best Local Similarity 93.8%;
Matches 412; Conservative
                                                                                               Query Match
                                                                                                                                               LENGTH: 439
TYPE: PRT
ORGANISM: homo sapiens
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nes 412; Conserv
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                                                                 Conservative
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93.8%;
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APPLICANT: Leiby, Kevin R.

APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Kapeller-Libermann, Maria A.

TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
CURRENT APPLICATION NUMBER: US/10/012,140
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR PILING DATE: 2000-11-15
PRIOR PILING DATE: 2000-11-15
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LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
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SOFTWARE: FastSEQ for Windows Version
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tch 98.3%; Score 2088; DB 26; Length 414; al Similarity 98.3%; Pred. No. 1e-210; 407; Conservative 3; Mismatches 4; Indels 0
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В	Ş	Дb	Ş	DB DB	Ş	DЬ	Ş
361	361	301	301	241	241	181	181
361 IMIAWNGIERLRAGLGILHDIEGIRYBPKCPLGVDISKEVGEASIKVPQLKMEI 414	361 IMIAWNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI 414	301 THRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALBILTNATQCTLLCPPPRLCTDNG 360	301 THRAILECKORDLLPQNNAVLVASGGVASNEYIRRALEILTNATOCTLLCEPPRLCTDNG 360	PPLHHAKNCDPSFTGLQHVTDKNNENRKQEEGIEKGQILSSAADIAATVQHTMACHLVKR 300	PPLHHAKNCDFSFTGLQHVTDKIIMKXEKEEGIEKGQILSSAADIAATVQHTMACHLVKR 300	181 QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK 240	181 QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK 240

Search completed: February 16, 2005, 13:18:55 Job time : 229.8 secs

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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*

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6 US-10-436-718-6 US-10-450-763-4045 6 US-10-805-075-2 6 US-10-805-075-4 8 US-60-643-717-274 8 US-60-643-717-12461 8 US-10-450-763-37549 6 US-10-450-763-37549 7 US-11-031-175-13545 7 US-11-027-399-5050 7 US-11-027-893-5050	480	480	480	480	480	480	480	480	480	480	480	612	1184	1073	398	398	917	917	852	
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## ALIGNMENTS

US-11-027-399-4857; Sequence 4857, Application US/11027399

GENERAL INFORMATION:
APPLICANT: Doucette-Stamm,

APPLICANT:

Bush, David

```
APPLICANT: Zeng, Qiandong
APPLICANT: Opperman, Timothy
APPLICANT: Opperman, Timothy
APPLICANT: Houseweart, Chad Eric
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: 3687.1000-015
CURRENT APPLICATION NUMBER: US/11/027,399
CURRENT APPLICATION NUMBER: US 10/640,833
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR APPLICATION NUMBER: US 09/583,111
PRIOR APPLICATION NUMBER: US 09/583,111
PRIOR APPLICATION NUMBER: US 09/583,111
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-07-07-02
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; SEQ ID NO 4857
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-11-027-399-4857
                                                                                                                                                                                                                                                                                                                                                                            Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                    / Match 21.3%; Score 453; DB 7;
Local Similarity 34.2%; Pred. No. 1.2e-33;
                                                                                                                                                         4 RYILAFETSCOETSVAVLKNODELLSNVIASQIESHKRFGGVVPEVASRHHVEVITACIE
STMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKG
                                                      SVEPLEFPLLALLVSGGHTELVYVSEAGDYKIVGETRDDAVGEAYDKVGRVMGL-----
                                                                                  LTWKVBFFFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPBC
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 336;
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CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
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APPLICANT: Doucette-Stamm, Lynn
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Best Local Similarity
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LENGTH: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
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TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: 3687.1000-024
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                                                                                                                                                                                                                                                                                                                        124 SVEPLEFPLLALLVSGGHTELVYVSEAGDYKIVGETRDDAVGEAYDKVGRVMGL-----
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                                                                                                                                                                                              QILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRA 336
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                                                                   L--AAEITDVKVIIPPLRLCGDNAGMIAYASVSEWN
                                                                                                             LEILTNATQCTLLCPPPRLCTDNGIMIA-----WN 366
                                                                                                                                                    ESLST-EDLCASFQAAVMDILMAKTKKAL-----EBYPVK--TLVVAGGVAANKGLRER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.3%; Score 453; DB 7; Length 336; 34.2%; Pred. No. 1.2e-33; tive 57; Mismatches 134; Indels
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APPLICANT: Bush, David
APPLICANT: Zeng, Qiandong
APPLICANT: Opperman, Timothy
APPLICANT: Houseweart, Chad Eric
TITLE OF INVENTION: Nucleic Acid and Amino Acid
TITLE OF INVENTION: Pneumoniae for Diagnostics
FILE REFERENCE: 3867.1000-010
CURRENT APPLICATION NUMBER: US/11/028,169
CURRENT FILING DATE: 2004-12-30
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US-11-028-169-4857
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                        Sequence 4857, Application US/11028169 GENERAL INFORMATION:
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LENGTH: 336
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PRIOR FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
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TITLE OF INVENTION: Nucleic Acid amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: 3687.1000-008
CURRENT APPLICATION NUMBER: US/11/027,878
CURRENT FILING DATE: 2004-12-30
APPLICANT: Doucette-Stamm,
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ORGANISM: Streptococcus pneumoniae
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Zeng, Qiandong
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34.2%; Pred. No. 1.2e-33;
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Sequences Relating to Streptococcus and Therapeutics

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RESULT 5
US-11-028-204-4857
; Sequence 4857, Applic
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
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SEQ ID NO 4857
LENGTH: 336
NUMBER OF SEQ ID NOS:
SEQ ID NO 4857
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CURRENT APPLICATION NUMBER: US/11/028,204
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Opperman, Timothy
APPLICANT: Opperman, Timothy
APPLICANT: Houseweart, Chad Bric
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
                                                                                                PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR PILING DATE: 1998-05-12
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                                                  PRIOR APPLICATION NUMBER: US 60/051,553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEILTNATQCTLLCPPPRLCTDNGIMIA-----WN 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zeng, Qiandong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lynn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 453; DB 7;
Pred. No. 1.2e-33;
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US-11-027-877-4857
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; ORGANISM: Stre
US-11-028-204-4857
                                                                                                                                                                                                                                                                                                SEQ ID NO 4857
LENGTH: 336
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                                                                                                                                                                                  Query Match
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Best Local
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APPLICANT: Opperman, Timothy
APPLICANT: Houseweart, Chad Bric
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: 3687.1000-022
CURRENT APPLICATION NUMBER: US/11/027,877
CURRENT APPLICATION NUMBER: US/11/027,877
PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR PILING DATE: 2003-08-14
                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
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                                                                                                                                                                                                                                                                                  TYPE: PRT
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Local Similarity 34.2%; Pred. No. 1.2e-33;
hes 115; Conservative 57; Mismatches 134;
                                                                                                                                                              Local
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                                                                                                                                    tch 21.3%; Score 453; DB 7; I al Similarity 34.2%; Pred. No. 1.2e-33; l15; Conservative 57; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
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97 RALSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIR 156
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                                             RYILAFETSCDETSVAVLKNDDELLSNVIASQIESHKRFGGVVPEVASRHHVEVITACIE 63
                                                                *IVLGIETGCDDTAAAVVUBTGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQ 96
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                                                                                                                                                                                  Length 336;
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; SEQ ID NO 4857
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-11-027-879-4857
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CURRENT APPLICATION NUMBER: US/11/027,879

CURRENT PILING DATE: 2004-12-30

PRIOR APPLICATION NUMBER: US 10/640,833

PRIOR FILING DATE: 2003-08-14

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 1998-06-30

PRIOR PILING DATE: 1998-06-30

PRIOR PILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR PILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR FILING DATE: 1997-07-02
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APPLICANT: Bush, David
APPLICANT: Zeng, Qiandong
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TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
                   277
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                                                                                                                               124 SVEPLÉFPLLALLVSGGHTELVYVSEAGDYKIVGETRDDÁVGEAYDKVGRVMGL-----
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 QILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRA 336
                                                     -TYPAGREIDELAHQGQDI-YDFPRAMIKEDNLEFSFSGLKSAFINLHHNAE-----QKG
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                                                                                                                                                                                                                                                                                                                                             21.3%; Score 453; DB 7; Length 336
34.2%; Pred. No. 1.2e-33;
tive 57; Mismatches 134; Indels
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               US-11-027-802-4857

Sequence 4857, Application US/11027802

GENERAL IMPORMATION:

; APPLICANT: Doucette-Stamm, Lynn
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LENGTH: 336
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Bush, David
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; TYPE: PRT ; ORGANISM: Streptococcus pneumoniae US-11-028-149-4857
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; Sequence 4857, Application US/11028149
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CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR PILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: US 09/107,433
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR PILING DATE: 1998-05-12
PRIOR PILING DATE: 1998-05-12
PRIOR PILING DATE: 1997-07-02
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Houseweart, Chad Eric TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics FILE REFERENCE: 3687.1000-017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 5322
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                                                                                                                                                                                                                                                                                                                                                                                                              231 ESLST-EDLCASFQAAVMDILMAKTKKAL-----EEYPVK--TLVVAGGVAANKGLRER 281
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L--AABITDVKVIIPPLRLCGDNAGMIAYASVSEWN
                                                         LEILTNATQCTLLCPPPRLCTDNGIMIA-----WN 366
                                                                                                                                                                                    QILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRA 336
                                                                                                                                                                                                                                                 -TYPAGREIDELAHOGODI-YDFPRAMIKEDNLEFSFSGLKSAFINLHHNAE-----QKG
                                                                                                                                                                                                                                                                                                              STMSGGKAIEHLAKOGNRFHFDIKPPLHHAKNCDFSFTGLOHVTDKIIMKKEKEEGIEKG
                                                                                                                             ESLST-EDLCASFQAAVMDILMAKTKKAL-----EBYPVK--TLVVAGGVAANKGLRER
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Opperman, Timothy
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APPLICANT: HOUSEWeart, Chad Eric
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: 3687.1000-011
CURRENT APPLICATION NUMBER: US/11/027,802
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR FILING DATE: 2003-08-14
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR PILING DATE: 1998-05-12
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PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR SEQ ID NOS: 5322
SEQ ID NO 4857
LENGTH: 336
TYPE: PRT
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GENERAL INFORMATION:
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                        FILE REFERENCE: 3687.1000-020
CURRENT APPLICATION NUMBER: US/11/027,890
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR PILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                         APPLICANT: Doucette-Stamm, Lynn
APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Zeng, Qiandong
APPLICANT: Opperman, Timothy
APPLICANT: Houseweart, Chad Bric
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
APPLICATION NUMBER: US 09/107,433
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34.2%; Pred. No. 1.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57; Mismatches 134; Indels 30;
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CURRENT APPLICATION NUMBER: US/11/027,892
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-05-12
PRIOR PILING DATE: 1998-05-12
PRIOR PILING DATE: 1997-07-02
NUMBER: OF SEQ ID NOMBER: US 60/051,553
PRIOR PILING DATE: 1997-07-02
NUMBER: OF SEQ ID NOS: 5322
SEQ ID NO 4857
LENGTH: 336
TYPE: PRIOR PILING DATE: 1997-07-02
NUMBER: OF SEQ ID NOS: 5322
SEQ ID NO 4857
LENGTH: 336
TYPE: SET
ORGANISM: Streptococcus pneumoniae
US-11-027-892-4857
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PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR ETILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 4857
LENGTH: 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4857, Application US/11027892 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Houseweart, Chad Bric TITLE OF INVENTION: Nucleic Acid amino Acid Sequences Relating to Streptococcus TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics FILE REFERENCE: 3687.1000-009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Doucette-Stamm, Lynn
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34.2%; Pred. No. 1.2e-33;
ative 57; Mismatches 134
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Query Match

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Best Local Similarity
Matches 115; Conserv
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LENGTH: 336
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APPLICANT: Houseweart, Chad Eric
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: 3687.1000-019
CURRENT PPLICATION NUMBER: US/11/028,099
CURRENT FILING DATE: 2004-12-30
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PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR FILING DATE: 2003-08-14
PRIOR PELICATION NUMBER: US 09/583,110
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
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                                                                                                                                             RYILAFETSCDETSVAVLKNDDELLSNVIASQIESHKRFGGVVPEVASRHHVEVITACIE
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Opperman, Timothy
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57; Mismatches 134;
Indels
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR PRIOR PRIOR NUMBER: US 09/085,131
PRIOR ETLING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 4857
LENGTH: 336
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TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
PILE REFERENCE: 3687.1000-007
CURRENT APPLICATION NUMBER: US/11/028,197
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR PILING DATE: 2003-08-14
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115; Conserv
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                                                                                                                                                                       -TYPAGREIDELAHQGQDI-YDFPRAMIKEDNLEFSFSGLKSAFINLHHNAE-----QKG
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Opperman, Timothy
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34.2%; Pred. No. 1.2e-33;
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US-11-028-050-4857; Sequence 4857, Application US/11028050; GENERAL INFORMATION:
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SEQ ID NO 4857
LENGTH: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 115; Conservative
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HOUSE-weart, Chad Bric
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: 3687.1000-012
CURRENT APPLICATION NUMBER: US/11/027,844
CURRENT APPLICATION NUMBER: US 10/640,833
PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR FILING DATE: 2003-08-14
PRIOR FILING DATE: 2003-08-14
PRIOR FILING DATE: 2003-08-14
PRIOR FILING DATE: 2003-08-14
PRIOR PRIOR FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: US 09/583,110
                                                                             APPLICANT: Doucette-Stamm, Lyr
APPLICANT: Bush, David
APPLICANT: Zeng, Qiandong
APPLICANT: Opperman, Timothy
APPLICANT: Houseweart, Chad Eric
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
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PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
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APPLICANT: Bush, David
APPLICANT: Zeng, Qiandong
APPLICANT: Opperman, Timothy
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PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/085,131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 RYILAFETSCDETSVAVLKNDDELLSNVIASQIESHKRFGGVVPEVASRHHVEVITACIE
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34.2%; Pred. No. 1.2e-33;
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216

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FILE REFERENCE: 3687.1000-023
CURRENT APPLICATION NUMBER: US/11/028,050
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
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Best Local :
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282
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L--AAEITDVKVIIPPLRLCGDNAGMIAYASVSEWN
                                                                         LEILTNATQCTLLCPPPRLCTDNGIMIA-----WN 366
                                                                                                                                                                                                                                      QILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRA 336
                                                                                                                                                                                                                                                                                                                                                                 STMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKG
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                                                                                                                                                                                                                                                                                                                    -TYPAGREIDELAHQGQDI-YDFPRAMIKEDNLEFSFSGLKSAFINLHHNAE-----QKG
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63 96

Search completed: February 16, 2005, 13:19:29 Job time : 15.15 secs

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Result
No.
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-MODEL=frame+ p2n.model -DEV=xlh
-PROCALIGN=1 - 1/USTO spool/US10649273/runat 14022005 114702 16399/app query.fasta_1.1429
-DB=GenEmbl -QFMT=fastap -SUFFIX=ree -MINMATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR SCORE-pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10649273 @CGN 1 1 8655 @runat 140022005 114702 16399 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Sequence:
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                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                               Query
Score Match Length DB
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2125 100.0
2125 100.0
090.5 98.4
090.5 98.4
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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2125
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Copyright (c) 1993 - 2005 Compugen Ltd.
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BC011904 Homo sapi
AR428803 Sequence
AR428808 Sequence
AJ295148 Homo sapi
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## ALIGNMENTS

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	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BC011904 LOCUS DEFINITION
Atlaschal, S.P., Zeeberg, B., Wagner, L., Shemmen, C.M., Schuler, C.D., Altschal, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.P., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richarde, S., W., Willalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Glbbs, R.A., Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,	Mammalia, Butheria, Primates, Ctanidata; vertebrata; Eurereoscom; Mammalia, Butheria, Primates, Ctatarrhini, Hominidae, Homo.  1 (bases 1 to 1908)  Strausberg,R.L., Peingold,B.A., Grouse,L.H., Derge,J.G., Viausberg,R.L., Peingold,B.A., Grouse, Charles G. Chuler G. D. Chuler G. Chuler G. D. Chuler G. Chuler	BC011904.2 GI:40225818  RC011904.2 (human)  Homo sapiens (human)  RC011904.2 (human)	BC011904 1908 bp mRNA linear PRI 23-DEC-2003 Homo sapiens O-sialoglycoprotein endopeptidase-like 1, mRNA (CDNA

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Alignment Scores:
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REFERENCE
AUTHORS
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Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beufstome,Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.B., Jones,S.J. and Marra,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (30-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Contact: MGC help desk
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NIH-MGC Project URL: http://mgc.nci.nih.gov
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                                                 ThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaVal 320
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                                                                                                                                    SerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArg
                                                                                                                                                                                                   GATAAAATAATAATGAAAAAGGAAAAAGGGAAGGTATTGAGAAGGGGCAAATCCTGTCT
                                                                                                                                                                                                                            AspLysIleIleMetLysLysGluLysGluGluGlyIleGluLysGlyGlnIleLeuSer
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583 160 523 140 463 120 403 100 343 90 283 60 223 40

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SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 1387) AUTHORS Chen,J., Feder,J.N., Nelson,T.C., Krystek,S.R. and Duclos,F.	Db 471 CCAGCAGCTCAACAGCTTCACAGAGAAATATTCAACGAATAGTACAAGAAGCTCTTTCT 530  Qy 101 AlaSerGlyValSerProSerAspLeuSerAlaIleAlaThrThrIleLysProGlyLeu 120
RESULT 3 AR428808 AR428808 LOCUS AR428808 DEFINITION Sequence 21 from patent US 6642041. ACCESSION AR428808 VERSION AR428808.1 GI:40188594 KEYWORDS .	Qy 61 LeuGlyGluAlaIleHisSerGlnThrGluValHisLeuLysThrGlyGlyIleValPro 80
Qy 401 GlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 414	41 GlylleGluThrSerCysAspAspThrAlaAlaAlaValValAspGluThrGlyAsnVal 60 
Qy 381 IleGluGlyIleArgTyrGluProLysCysProLeuGlyValAspIleSerLysGluVal 400	21 GlupheLeuArgSerpheAsnpheHisproGlyThrLeuPheLeuHisLysIleValLeu 4 
Oy 361 IleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAsp 380	1 MetLeuIleLeuThrLysThr 
Qy 341 ThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGly 360	100.00% Indels: 6 Gaps: 6 Gaps:
Oy 321 LeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeu 340	Allgiment Scores: 7.37e-171 Length: 2197 Pred. No.: 2125.00 Matches: 414 Score: 2125.00 Matches: 0 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0
Oy 301 ThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaVal 320	ORIGIN /mol_type="genomic DNA"
Qy 281 SerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArg 300	Patent: US 6642041-A 1 04-NOV-2003; Location/Qualifiers 12197 ce /organism="unknown"
Qy 261 AspLysIleIleMetLysLysGluLysGluGluGlyIleGluLysGlyGlnIleLeuSer 280	
Qy 241 ProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThr 260	
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Qy 201 LeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCysSerThrMetSer 220	04 GGAGAAGCTTCCATAAAAGTACCACAATTAAAAATGGAGATA
Qy 181 GlnGlyValSerAspPheLeuLeuGlyLysSerLeuAspIleAlaProGlyAspMet 200	1244 ATAGAAGGCATCCGCTATGAACCAAAATGTCCTCTTGGAGTAGACATATCAAAAGAAGTT 1
Oy 161 ValGluPheProPheLeuValLeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuVal 180	Db 1184 ATTATGATTGCATGGAATGGTATTGAAAGACTACGTGCTGGGCATTTTACATGAC 1243  OV 381 IleGluGlvI]eArgTvrGluProLvsCvsGVrOLeuGlvVallasnTleSerIvsGluVal 400
Qy 141 PropheileProlleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAsnLys 160	341 InrasnalaThroincysfinrLeubeucysproProPargleucysfinrAspAsnGly 3
Oy 121 AlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeuLysLys 140	321 LeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeu 3

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1. 1387
                                                                                                        GlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLys
                                                                                                                                                    LeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCysSerThrMetSer
                                                                                                                                                                                                   GlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAlaProGlyAspMet
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            AspLysIleIleMetLysLysGluLysGluGluGlyIle----
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GATAAAATAATAATGAAAAAGGAAAAAGAGGAAGGTATATTTCTAATTAGTAAAGTTGAA
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                                                                                            GGTGGGAAAGCCATAGAGCATTTGGCCAAACAAGGAAATAGATTTCATTTTGACATCAAA
                                                                                                                                         CTTGACAAGGTGGCAAGAAGACTTTCTTTAATAAAACATCCAGAGTGCTCCACCATGAGT
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Homo sapiens mRNA for putative s
Au7295148
Au7295148.1 GI:11071726
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Submitted (27-OCT-2000) Chen J.M.,
Laboratory, The Babraham Institute,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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24. .1343
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GCCAGTGGAGTCTCTCCAAGTGACCTCTCAGCAATTGCAACTACCATAAAACCAGGACTT

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                  Homo sapiens (human)
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Sequence 400 from Pateni
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     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
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Full-length cDNAs
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Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makta, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wayatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Shiratori, A., Sudo, H., M., Nanda, K., Yokoi, T., Furuya, T., Kikkawa, B., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Satoo, K., Kakuka, R., Omura, Y., Jah, K., Ishibashi, T., Yamashita, H., Mirakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hitaoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yoshida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aoteuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Moniyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Sujiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, T., Sujiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Kowabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Nobatake, N., Inagaki, H., Jikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Kobatake, N., Inagaki, H., Shigata, K., Senba, T., Matsumura, K.,
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Homo sapiens (human)
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2208 bp mRNA linear PRI 30-JAN-2004
Homo sapiens cDNA FLJ30879 fis, clone FEBRA2004592, highly similar
to Homo sapiens mRNA for putative sialoglycoprotease type 2.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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TITLE
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REFERENCE
                                                            Query Match:
DB:
US-10-649-273-2 (1-414) x AK055441 (1-2208)
                                                                                                                Best Local Similarity:
                                                                                                                                                                               Score:
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Direct Submission

Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,

Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

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NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: RAB and
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NSGGKAIEHLAKQGNRFHFDIKEPLHLAKNCDFPFTGLQHVTDKIIMKKEKEBGIEKG
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                      IleGluGlyIleArgTyrGluProLysCysProLeuGlyValAspIleSerLysGluVal 400
                                                                                                    IleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAsp
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                                                                                                                                                                                                                                                                 LeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeu
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                                                                                                                                                                                                                                        CIGGTIGCATCIGGIGGIGGICGCAAGIAACTICIGTATCCGCAGAGCICIGGAAATTITA 1363
                                                                                                                                                                                                                                                                                                                      ACACATCGGGCTATTCTGTTTGTAAGCAGAGAGACTTGTTACCTCAAAATAATGCAGTA
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-TGATGTCCTCTTGGAGTAGACATATCAAAAGAAGTT 1471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RS Strausberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Wyers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,
Generation and initial analysis of more than 15,000 full-length
human and mouse CDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1472
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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consorcium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 123 Row: d Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 2131240 Location/Qualifiers
                                                                                                                                                                                                                                      web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Dietrich,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (15-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg, R.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                             AlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeuLysLys
                                                                                                                                         AlaSerGlyValSerProSerAspLeuSerAlaIleAlaThrThrIleLysProGlyLeu
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                                                                                                                                                                                                                                                                                                                                                                    GluPheLeuArgSerPheAsnPheHisProGlyThrLeuPheLeuHisLysIleValLeu
                  ProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAsnLys 160
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                                                             GCCCTAAGCTTAGGAGTCGGCTTATCCTTTAGCTTACAGCTAGTAAAATCGGTTTAAAAAG
                                                                                                                         GCCAGTAGAATCACCCCAAGCGATCTCTCGGCAATTGCAACTACCATCAAACCGGGACTG
                                                                                                                                                                                     CCAGTAGCTCAACAACTTCACAGAGAAAATATTCAACGAATAGTAGAAGAAACTCTTTCT
 TTCATCCCGATTCATCACATGGAGGCTCACGCACTGACTATTAGGCTCACCAATAAA
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possible chaperone activity [Posttranslational
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333. .1397
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QILSSAADIAAAVQHATACHLAKRTHRAILFCKQKNLLSPANAVLVVSGGVASNLYIR
KALEIVANATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGVLHDVEDIRYEPKCPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MLMLRRTAGAIDKEPKSKYVGFLRRFSVHPRTLSCHKLVL/GIET
SCDDTGAAVVDETGNVLGEALHSQTQVHLKTGGIVPPVAQQLHRENIQRIVEETLSAS
RITPSDLSAIATTIKPGLALSLGVGLSFSLQLVNRFKKPFIPHHMEAHALTIRLTNK
VEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modification, protein turnover, chaperones]"
/db_xref="CDD:COG0533"
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/product="Unknown (protein
/protein_id="AAH58172.1"
/db_xref="GI:34849664"
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/clone="MGC:67870 IMAGE:5012054"
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                                                                                                                                                                                                                AR541929
Sequence 17
AR541929
AR541929.1
                                                                                      1 (bases 1 to 1416)
Tang,Y.T., Zhou,P., Goodrich,R., Liu,C.,
Zhang,J., Zhao,Q.A., Yang,Y., Xue,A.J., V
Wang,D. and Drmanac,R.T.
                                          Nucleic acids and polypeptides
Patent: US 6743619-A 177 01-JUN-2004;
Location/Qualifiers
                                                                                                                                                                     Unknown
                                                                                                                                                     Unclassified.
                                                                                                                                                                                     Unknown
                                                                                                                                                                                                                                                                                                                        GlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 414
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GCAGAAGCTGCCATAAAAGTACCGCGATTAAAAATGGCACTT 1463
                                                                                                                                                                                                                                                                                                                                                                                  IleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAsp 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGly 360
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GlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGly 393
                                                                                                                                                                                                                                             GluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMet
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                                                                                                                                                                                             AlaCysHisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeu 313
                                                                                                                                                                                                                                                                                            ThrGlyLeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIle 273
                                                                                                                                                                                                                                                                                                                                             ArgPheHisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPhe 253
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                       ArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAla 373
                                                                                      ArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProPro 353
                                                                                                                                                     LeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIle 333
                                                                                                                                                                                                                                                                                 AGATTTCATTTTGACATCAAACCTCCCTTGCATCATGCTAAAAATTGTGATTTTTCTTTT 819
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                        CDNA Library Preparation: Express Genomics CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, Web site:

http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Director MGC Project.

Direct Submission

Submitted (02-NUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1546
Rattus norvegicus cDNA clone
BC078974
                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Scrice: IRAK Flate: 182 Row: f Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Howard Jacobs
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Mammalia; Butheria;
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IMAGE:7111906, partial
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GlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAlaProGlyAspMet
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                                                      GTCGGATTTCCTTT
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RIUSHRVLTALTEDLDSVSSTHTVAHSPLNSGSRGANIQTSMCSCTQTVYMRTVRHTL
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/clone="IMAGE:7111906"
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RESULT 12
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Sequence 23 from patent
AR428809
AR428809.1 GI:40188595
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Chen, J., Feder, J.N., Nelson, T.C., Krystek, S.R. and Duclos,
Polynucleotides encoding a novel metalloprotease, MP-1
Patent: US 6642041-A 23 04-NOV-2003;
                                                                                                                                                                                                                                                                                                             Unknown
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  MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal 167
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1 (bases 1 to 1522)
Boardman, P.B., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk Croning, M.D.R., Davies, R.H., Francis, M.D., Grafham, D.V., Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren Niblett, D., Overton, I.M., Rogers, J., Scott, C.B., Taylor, R.G. Tickle, C. and Wilson, S.A.
                                                                                                                                       Gallus gallus (chicken)
Gallus gallus
                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire,
Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
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This sequence is from the
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                                  SerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHis
                                                                           ProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCys
                                                                                                                                     GlnLeuLysLysProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Gallus gallus"
/mol type="mRNA"
/strain="Layer and broiler"
/db xref="taxon:9031"
/clone="ChEST189114"
                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="CSEQRBN11"
/dev_stage="adult"
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                                                                                                                           Strausberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

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McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.B.,

Generation and initial analysis of Force than 15,000 full.length
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                                                                    human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAspIle
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      (bases 1 to 1017)
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Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin,
Susanna Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
Michael Thorne, Miranada Tsai, Matasja van den Bosch, Jill Vardy,
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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Submitted (25-OCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAK Plate: 86 Row: f Column: 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                             LysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisVal
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/mol_type="mRNA"
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/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B"
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/clone="IMAGE:5053559"
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1 (bases 1 to 1558)

Boardman, P.B., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S.E., Croning, M.D.R., Davies, R.M., Francis, M.D., Grafham, D.V., Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren, S.R., Niblett, D., Overton, I.M., Rogers, J., Scott, C.B., Taylor, R.G., Tickle, C. and Wilson, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EX930963
Gallus gallus finished (
BX930963
EX930963.2 GI:46016890
                                                                                                                                                                                                                                                                     Submitted (29-MAR-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: Chickest@bms.umist.ac.uk
On Apr 1, 2004 this sequence version replaced gi:41631491.
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
                                                                                                                                          and poly A-trimmed. EcoRI-NotI cut cDNA was then ligated into the vector. Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host: Escherichia coli DH10B.
                                                                                                                                                                                       BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST from a library constructed by Elizabeth Bosch. from RNA extracted from limbs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                         This sequence is from the
                                                                                                                                                                                                                                                      sequencing project
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              /mol_type="mRNA"
/strain="White Leghorn, H
/db_xref="taxon:9311"
/clone="Ch85762n16"
/clone_lib="CSEQCHL20"
                                                                                              organism="Gallus gallus"
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 dev_stage="stage 36"
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                                             ArgieuCysThrAspAsnGlyIieMetIieAlaTrpAsnGlyIleGluArgLeuArgAla 373
                                                                                                                          ArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProPro
                                                                                                                                                                                                                         GCTGCTCATATTATCCAGCGGACACACCGAGCCATGCTCTTCTGCATGAAAAAACAGCATA 1205
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                                                                                              AGAAAAGGACTGCAGACTCTGGCAAATGCAAACGGTTTTGCTTTTCTGTCTCCTCCTCCA
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Result
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-Q=/cgn2 1/USPTO_spool/US1649273/runat_14022005 114702 16389/app_query.fasta_1.1429
-Q=/cgn2 1/USPTO_spool/US1649273/runat_14022005 114702 16389/app_query.fasta_1.1429
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pc0 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10649273 @CGN 1 1 1057 @runat_14022005 114702 16389 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O-sialogycoproteinase-like protein and encoding polynucleotide, useful for diagnosing, preventing and treating related diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes an isolated nucleic acid molecule (I) encoding a cometalloprotease (WP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder, an aberrant glutamate transport or motor neuron disorder, such as a myotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like condition. The compositions and methods are also useful for diagnosing, prognosticating, treating, ameliorating and/or treating disorders group sociated with MP-1 activity, e.g. diabetes, cancer, reproductive disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell aplasia), metabolic disorders (e.g. premature puberty, Kallman syndrome, or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, Parkinson's disease, Huntington's disease or Tourette syndrome), liver and renal diseases and immune disorders (e.g. AIDS, rheumatoid arthritis or sepsis), pulmonary diseases (e.g. AIDS, rheumatoid arthritis or sepsis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This sequence represents a metalloprotease MPI polynucleotide
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US-10-649-273-2 (1-414) x ABT23207 (1-2572)

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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                          CC The invention relates to an isolated polypeptide comprising: any of 28 CC sequences of 48-1256 amino acids; a natural amino acid sequence at least CC 90% identical to the 28 amino acid sequences, 94% identical to a sequence CC of 703 or 267 amino acids, 96% identical to a sequence of 414 amino CC acids, or 97% identical to a sequence of 422 amino acids, all given in CC the specification; or a biologically active or immunogenic fragment of CC the isolated polypeptide. The polypeptides and polymucleotides are useful in diagnosing, treating and preventing diseases or conditions associated CC with the decreased expression of protein modification and maintenance CC molecules (PMOD), such as cell proliferative diseases (e.g. cancer, CC allergies), neurological disorders (e.g. stroke, Parkinson's disease, CC epilepsy), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g. crocer, crocer), and CC infections (e.g. bacterial, viral, parasitic, proctozoal). These are also CC concertial in assessing the effects of exogenous compounds on the expression CC fragments are useful in screening compounds for effectiveness as agonist CC or antagonist of the polypeptides, or in altering the expression of the activity of the polypeptides. The microarray is useful in monitoring CC crocering a human PMOD protein of the invention
                                                                                                        Alignment
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06-JUL-2001; 2001US-0303445P.
13-JUL-2001; 2001US-0305405P.
09-AUG-2001; 2001US-0311442P.
24-AUG-2001; 2001US-0314821P.
29-AUG-2001; 2001US-0315992P.
03-MAY-2002; 2002US-0378205P.
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protein-protein interaction; drug-target interaction;
gene expression profile; human; gene; ds.
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The present invention relates to novel 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules which encode adenosine deaminase, glycoprotease or seven transmembrane domain (?TM) receptor family members. Sequences of the invention are useful in diagnosing and treating cancer or aberrant cellular proliferation and/or differentiation (e.g. colon or lung cancer), immune disorders (e.g. selective IgA deficiency, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                     New 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules, useful for diagnosing and treating cancer, immune, cardiovascular, hematopoietic, brain, pain, metabolic, liver or platelet disorders, and the state of the 
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                                                                                                                                                                                                                                                                                                  Claim 1;
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Alignment

BP; 543 A; 365 C;

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The invention relates to an isolated 38650 (encoding adenosine CC deaminase), 28472 (encoding a glycoprotease), 5495 (encoding a 7 CC transmembrane receptor), 65507, 81588 or 14354 nucleic acid molecule (or cransmembrane receptor), 65507, 81588 or 14354 nucleic acids or cCC a sequence which is at least 60% identical to the six nucleic acids or their open reading frames, fragments of at least 15 nucleotides, CC naturally occurring variants, or a DNA insert of the plasmid deposited CC with the American Type Culture Collection as Accession No. not defined in CC the specification, which encodes the amino acid sequence). Also included are a host cell containing the nucleic acids (used to produce the protection), the encoded proteins, an antibody that selectively binds to CC the polypeptide, and identifying a compound that binds to/modulates the CC entivity of the polypeptide. The nucleic acid molecules, polypeptides and CC methods are useful for diagnosing, treating cancer, aberrant cellular CC proliferation and/or differentiation, immune disorders, heart disorders, CC cardiovascular disorders including endothelial cell disorders, pain CC and metabolic disorders, blood vessel disorders, brain disorders (many camples of these disorders are given in the specification). The present cycle sequence is the Human cDNA 28472 encoding a glycoprotease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated 38650, 28472, 5495, 65507, 81588 and 14354 nucleic acid molecules, useful for diagnosing, treating cancer, pain, or immune, heart, endothelial cell, hematopoeitic, blood vessel, brain, metabolic
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Cancer; aberrant cell proliferation; aberrant cell differentiation; breast cancer; ovarian cancer; prostate cancer; cardiovascular disorder; lung cancer; immune disorder; heart disorder; cardiovascular disorder; endothelial disorder; heatopoietic disorder; blood vessel disorder; brain disorder; metabolic disorder; liver disorder; diabetes; platelet disorder; carcinoma; sarcoma; leukaemia; Hodgkin's disease;
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WPI; 200
P-PSDB;
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                                                                                                                                                                                                                                                                                                                                08-NOV-2000; 2000US-0246768P
08-NOV-2000; 2000US-0246772P
15-NOV-2000; 2000US-0249185P
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myocardial infarction; ischaemic heart disease; Crohn's disease;
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/product= "Glycoprotease 28472"
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New adenosine deaminase, glycoprotease and seven transmembrane nucleic acids and polypeptides, designated 38650, 28472, 5495, 81588 and 14354, useful for treating e.g. leukemias, Hodgkin's 65507, disease õ

Claim 2; Fig 8A-B; 178pp; English

CC The invention describes isolated 38650, 28472, 5495, 65507, 81588 and CC 14354 nucleic acid molecules (I) and their encoded polypeptides (II). The CR 38650 nucleic acid molecule comprises a sequence encoding adenosine CC deaminase. The 28472 nucleic acid molecule comprises a sequence encoding adenosine CC sequences that encode a human seven transmembrane domain (7TM). The CR 3850, 28472, 5495, 65507, 81588 and 14354 comprise CC sequences are useful for diagnosing, preventing or treating a subject CC with or at risk of developing a disorder, e.g. cancer or aberrant CC with or at risk of developing a disorder, e.g. cancer or aberrant CC collular proliferation and/or differential disorders, heart disorders, collular proliferation and/or differential disorders, heart disorders, brain disorders, pain and metabolic disorders, CC cardiovascular disorders, endothelial disorders, heart disorders, colliver disorders or platelet disorders. These disorders include carcinoma, sarcoma, leukaemia, Hodgkin's disease, autoimune disorders, Kawasaki CC ischaemic heart disease, Crohn's disease, autoimune disorders, Kawasaki CC ischaemic heart disease, aneurysm, cerebral ischaemia, peripheral concachexia or diabetes. This sequence encodes the novel human glycoprotease.

Sequence 1821 543 A; 365 ü 394 ଦ 518 Η. 0 1 Other;

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US-10-649-273-2 (1-414)× ABS57020 (1-1821)

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IleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAsp
                                       LeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeu
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US-10-649-273-2 (1-414) x ADA52832
                                                                                                                                                                                                                                                                                    The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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P-PSDB; ADA54471.
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24-JAN-2002; 2002US-0350435P.
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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Example 2; SEQ ID NO 7447; 210pp; English

The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression in the first soft tissue samples and comparing the expression in the first soft tissue samples the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.

Sequence 2890 BP; 869 A; 609 ü 611 G; 789 T; 0 U; 12 Other;

Percent Similarity:
Best Local Similarity:
Query Match:
DB: Score: US-10-649-273-2 (1-414) x ADQ24627 (1-2890) Pred. No.: Alignment Scores: 3.2e-193 1944.00 93.24% 93.24% 91.48% Conservative: Mismatches: Indels: Gaps: Length: Matches:

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Drmanac RT,
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Novel polypeptide useful for treating neurodegenerative diseases, myeloid or lymphoid cell disorders, bone disorders, mechanical and traumatic disorders, coagulation disorders, and inflammatory diseases.

Claim 1; Page; 612pp; English

erythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus); myeloid or lymphoid cell disorders (e.g. anaemia and thrombocytopaenia); wounds, ulcers, burns; bone disorders (e.g. osteoprosis, osteoarthritis); mechanical and traumatic disorders (e.g. stroke, head trauma); lung or liver fibrosis; reperfusion injury in various tissues; bacterial, viral or fungal infections; allergic conditions such as allergic rhinitis, asthma; cosqulation disorders (e.g. heamophilia); cancer and tumours; and inflammatory diseases (e.g. heamophilia); infection or function of infectious agents such as bacteria, fungi, viruses, or to effect bodily characteristics, biorhythms or circadian cycles of rhythms. The protein may be used to inhibit the growth, cycles of rhythms. The protein may also have proliferation/differentiation, stem cell growth factor, haematopoiesis This invention relates to the cDNA sequences encoding an isolated novel human polypeptide. The protein encoded by the nucleic acid of the invention is useful for treating central and peripheral nervous system diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic lateral sclerosis); neurodegenerative diseases (e.g. Parkinson's disease, Alzheimer's disease); autoimmune disease (e.g. systemic lugus and the protein contract of the protein contr or suppressing, chemotactic/chemokinetic

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               ArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProPro 353
                                                                   LeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIle
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CGCAGAGCTCTGGAAATTTTAACAAACGCAACACAGTGCACTTTGTTGTGTCCTCCTCCC
                                                       TTACCTCAAAATAATGCAGTACTGGTTGCATCTGGTGGTGTCGCAAGTAACTTCTATATC
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The present invention describes a non-human transgenic animal (I) C comprising a disruption in a protease target gene (PG) selected from CC calcium activated neutral protease type 5 (CAPN5) gene, tryptase 4 gene CC and sialoglycoprotease-like gene. Also described is a targeting construct CC (II), comprising a first polynucleotide sequence homologous to at least a CC first portion of PG, a second polynucleotide sequence homologous to at CC least a second portion of PG and a selectable marker. (II) is useful for CC producing a transgenic mouse comprising a disruption in a protease target CC gene, by introducing (II) into a cell introducing the cell into a CC blastocyst, implanting the resulting blastocyst into a pseudopregnant course, where the pseudopregnant mouse gives birth to a chimeric mouse, CC and breeding the chimeric mouse to produce the transgenic mouse. (I) is useful for identifying an agenic that modulates the expression or function of a protease target gene, by administering an agent to (I) and cefficacy of proposed genetic and pharmacological therapies for human cc efficacy of proposed genetic and pharmacological therapies for human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel transgenic animal, comprising a disruption in protease target gene, is useful for identifying agents that ameliorates a phenotype associated with a disruption in a protease target gene.
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06-DEC-2000; 2000US-0251820P.
13-DEC-2000; 2000US-0255971P.
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SerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArg
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                                                                           CCACCTATGCAGAATGCTAAGAATTGCGATTTTTCTTTCACGGGACTTCAACATATTACT
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New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and

WPI; 2002-723329/78 P-PSDB; ABG96487.

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Feder J,

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BRISTOL-MYERS SQUIBB

05-FEB-2001; 2001US-0266518P. 10-APR-2001; 2001US-0282814P.

05-FEB-2002;

2002WO-US003353

19-SEP-2002 WO200272751-A2

Disclosure; Page 462-463;

473pp;

English

neurological

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            motor neuron disorder; mmotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; immune disorder; rheumatoid arthritis; acquired immunodeficiency syndrome; ALDS; pulmonary disease; pneumonia; emphysema; cystic fibrosis; vascular disorder; inflammatory disorder; neurological disorder; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metalloprotease; MP-1; immune disorder; glutamate transport; cancer;
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes an isolated nucleic acid molecule (I) encoding a metalloprotease (MP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder, an aberrant glutamate transport or motor neuron disorder, such as amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like condition. The compositions and methods are also useful for diagnosing, prognosticating, treating, ameliorating and/or treating disorders (e.g. kleinfelter's syndrome, genital warts, or germinal cell aplasia), metabolic disorders (e.g. premature puberry, Kalman syndrome, or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, Huntington's diseases (Alzheimer's disease, pulmonary disease (e.g. Tourette syndrome), liver and renal diseases and immune disorders (e.g. AIDS, rheumatoid arthritis or sepsis), pulmonary disease (e.g. perminal conspision), pulmonary disease (e.g. metalloprotease (e.g. Alzheimer's disease or Parkinson's disease). This sequence represents a metalloprotease MP1 polynucleotide
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                                                                                                                                                            CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal
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The invention relates to a novel isolated human diagnostic and therapeutic polynucleotide (designated dithp). The novel dithp polynucleotide comprises: any of 188 DNA sequences consisting of 195-7798 base pairs fully defined in the specification; a polynucleotide comprises of the dithp polynucleotide sequence at least 90% identical to the dithp polynucleotide; a polynucleotide sequence at least 90% identical; or an NNA equivalent of any of the polynucleotides mentioned above. The dithp polynucleotides have the following activities: antidiabetic, immunosuppressive, neuroprotective, nootropic, neuroleptic, tranquilizer, osteopathic, antiarthritic, antirheumatic, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnostic and therapeutic polynucleotide; dithp; antiarteriosclerotic; antiinflammatory; cerebroprotective; antilipaemic; antidiabetic; immunosuppressive; neuroprotective; nootropic; neuroleptic; tranquilizer osteopathic; antiarthritic; antirheumatic; cytostatic; hepatotropic; virucide; haemostatic; anti-HIV; antithyroid; thyromimetic; dermatological; antibacterial; fungicide; antiparasitic; anticonvulsant; thrombolytic; antibocagulant; anorectic; vasotropic; antiulcer; gene therapy; protein replacement therapy; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human diagnostic and therapeutic polynucleotides and polypeptides, useful for diagnosing, treating or preventing e.g. leukemia, brain cancer, atherosclerosis, AIDS, thyroiditis, infections, obesity, strok
                                                                                                                                                                                                                                                                                                                                                                                                                                                         or Alzheimer's.
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Kristnam SR,
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17-JAN-2002; 2002US-0349413P.
17-JAN-2002; 2002US-0349946P.
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CH, Lewis SA, Chen A,
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ap PE, Amshey SR, Dam
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m TC, Liu TF, Gerstin
t, Lan RY, Urashka ME;
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                                                                                                                                                                         US-10-649-273-2 (1-414) x ABL24633 (1-1601)
                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins (ABB5737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                Sequence 1601 BP; 344 A; 477 C; 441 G; 339 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 25372; 21pp + Sequence Listing; English.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                      ValLeuGlyIleGluThrSerCysAspAspThrAlaAlaAlaValValAspGluThrGly 58
                                                                                             GTCCTGGGCATCGAGACCTCCTGCGACGACACGGGCATCGCCATCGTGGACACCACGGGC 138
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                                     standard; cDNA;
                                                                                                                 AGCATTGATATCCAGGGCAGCGCGGGATTCGCC
                                                                                                                                                  GlyValAspIleSerLysGluValGlyGluAla 403
                                                                                                                                                                                                                  GlyLeuGlyIleLeuHisAspIleGlu---GlyIleArgTyrGluProLysCysProLeu 392
                                                                                                                                                                                                                                                                                        ArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAla 373
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CACCTGATGCACCGCAGCGGGCAATTGAGTACTGCCTCCTGCCGCACAGGCAGCTC
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Alignment
Pred. No.:
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                                                                                                                                                                           Percent Similarity:
Best Local Similari
                                                                                                                                                                                                                                                                                                                                                    of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end complementary to a polynucleotide which comprises a 3'-end sequence complementary to a complementary to complementary to a complementary to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1999; 99JP-00253.
27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer
length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isogai T,
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                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1616-ABL30511), expressed DNA sequences (ABL1616-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                  uCysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLe 375
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                                                                                                                  gAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLe
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Search completed: February 16, 2005, 13:58:31 Job time : 834.4 secs	1465 TGATATCCAGGGCAGCGCGGGATTCGCC 1438	394 lAspIleSerLysGluValGlyGluAla 403	1509CTGCAGGATAAAGAGGCCAGCACGCGCTACGACTACGACAGCAT 1466	375 uGlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyVa 394

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-LOOPEXT=0 -UNITS-bits -START=1 -EXD=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORS=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-USER=US10649273 @CGN 1 1_292 @runat 14022005 114704 16425 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPPEXT=7 -YGAPOP=10 -YGAPAXT=0.5 -DELOP=6 -DELEXT=7
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1. /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

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3. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4. /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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Sequence 38, Appl
Sequence 806, App
Sequence 801, App
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Percent Similarity:
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5.72e-261 2125.00 100.00% 100.00%

Length:
Matches:
Conservative:
Mismatches:
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1, Application US/10067443 1, Application US/10067443 1, 6642041 TT: Bristol-Myers Squibb Continuention: POLYNUCLEOTIDE INVENTION: POLYNUCLEOTIDE INVENTION: SPINAL CORD, PERRENCE: D0073 WABER: US/10/0 FILING DATE: 2002-02-05 FILING DATE: 2001-02-05 FILING DATE: 2001-02-05 FILICATION NUMBER: US 60/260 LING DATE: 2001-04-10 FILING DATE: 2001-04-10 FIRE DATE: 2001-04-10 FIRE DATE: 2001-04-10 FIRE SEQ ID NOS: 71 1: Patentin version 3.0		1315 1830121 1830121 1032 1008 1001 1006 1006 1007 1006 1007 1011 1011
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IleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAsp 380
                                                                                                                                  LeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeu 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; sequence 21, Application US/10067443; Patent No. 6642041; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
NUMBER: Patentin version 3.0
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Sequence 177, Application US/09774528
Patent No. 6743619
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Ann, Feiyan
APPLICANT: Ann, Jeiyan
APPLICANT: Zhang, Jing
APPLICANT: Zhang, Jing
APPLICANT: Yang, Yonghong
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APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
TITLE OF INVENTION: No. 6743619el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 177
LENGTH: 1416
TYPE: DNA
ORGANISM: Homo sapiens
FERTURE:
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Best Local Similarity:
Query Match:
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; LOCATION: (205)..(1305)
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITILE OF INVENTION: POLYNUCLEOTIDE ENCODING A
ITILE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT ELING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.0 SEQ ID NO 23
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TYPE: DNA
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                                                                                                                                                              APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A |
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILLNG DATE: 2002-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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US-10-067-443-20
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   Percent Similarity:
                                             Alignment
                                                                            US-10-067-443-20
                                                                                                                                                                                                                                                                                                                              sequence 20, Application US/10067443
Patent No. 6642041
GENERAL INFORMATION:
                                                                                                                                      SOFTWARE: PatentIn version 3.0 SEQ ID NO 20
                                                                                         LENGTH: 14364
TYPE: DNA
ORGANISM: homo
                                               Scores:
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2.19e-139
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12662 TCCAACTTTGGTGACACTAATGTTGATAAGTTCTGATAATCCACTATATTGTACCAGCC 12/21	TCAAGCCCATTTTCCAACCAATAGAAGAGCAAACATAGACAGGGGCAGTGATTGGCCTCT 11641	Db 11582 TCAAGCCCATTTTCCA
	204	Qy 204
2]	TAGGAAGTATAGGACAAGTTCTTATTATTGACGTTCATCATTAAGCAGTTATTGTCAACT 11581	Db 11522 TAGGAAGTATAGGACA
ממלים באיני בייניים באיני באינ	204 nh	Оу 204
42 GCAGTAACTGCTATCATTTTTAGAAAAATAGGTGGATTTCCTTCATCCTTTGATGAA	CATATATAGGAAAACAAACAAACAAACAAAACACTGCTTCCCCACAGTGAAATAA 11521	Db 11462 GCCATATATAGGAAAA
; ;	204	Qy 204
12482 AGTCTAATTTTGCATCTTCTTGGATTTAAAAGAGGGGCTTACAATAAAGAAAG	Db TACACCACAGACAGGGTCCCCCCCCCCCCCCCCTTTGTTTTAGAATACTACAGAGGCTACT 11461	Db 11402 TACACCACAGACAGGG
	204	Qy 204
22 CCATTTCTTGTACTAGTTTGGTAGCTTTATGGGACAGCTGTATAGCTTCTATGGCACATA	ATATAGATTAACATAAGGACATTAAAGATGCAATGCACAGAATTAAATCACACAATTACT 11401	11342
21	Qy 204	Оу 204
12362 CTTTATGCCTTATGCTAGCCCTGACAGTATGAAATTATGCAGGATAGGAAAGACTAACAG 12421	ATGTGAAAGAACGTGCTTCGTAAACTAACATACTGCAAAAAAAGGTAAAATAAGAGAATAT 11341	11282
321 321	AICIGIACAINAMGGCIGAAAINGITIGGAGAINAGGITAIGIAITITIGGGAAAIAAIGI 11281 Qy	DD 11222 AICIGIACATAAAGGC
12302 CACTTTGCAATATGTTACTTTTTTCCCCAAGACCTTGACCTTGTGTTTTAGGATGAACAGAT 12361	, ,	1 2 2
321 321		204
	204	204
12 pLeuLeuProGlnAsnAsnAlaValLeu	ATTTCTGAATTTTATCTTAGTAAACTGAAAAAATTCACATATGGTGAGAAAAAATAGA 11161 Qy	Db 11102 TATTTCTGAATTTTAT
	204 Db	Qy 204
92 rMeralaCvsHisLenValLvsArgThrHisArgAlalleLenDheCvsLvsGlnArgAs	TTGTTATGTTGTCCATTTCAACTAAGTAGCAATAGATGTGCTACCACCATTCACCTAAA 11101	Db 11042 TTTGTTATGTTGTCCA
TATTGAGAAGGGCAAATCCTGTCTTCAGCAGACATTGCTGCCACAGATACAGCAGAC	204 Db	Qy 204
12062 AAAGITIGAACAGATAAATATTICCIGGATTGTGCCTAAAAATAGCTGCTCATTTCTGCAGG 12121	GACATAGCACCAGGTGACATGCTTGACAAGGT-AATTAAGAATTAATTTCTCCATTCTTT 11041	Db 10983 GACATAGCACCAGGTG
	204	Qy 194 AspIleAlaProGlyA
02 CACGTTACTGATAAAATAATGAAAAAAGGAAAAAGAGGAAGGTATATTTCTAATTAGT	82	10923
258 HisValThrÄspLy8IleIleMetLysLysGluLysGluGlu 271		Qy 174 HisCysLeuLeuAlaL
11942 GACATCAAACCTCCCTTGCATCATGCTAAAAATTGTGATTTTTCTTTTACTGGACTTCAA 12001	ThrileargLeuThraanLygValGlupheProPheLeuValLeuLeuIleSerGlyGly 173	Qy 154 ThrIleArgLeuThrA
38 AspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGln	10862	
218 ThrMetSerGlyGlyLysAlalleGluHisLeuAlalySGlnGlyAsnArgPheHisPhe 237	Oy 	Qy 134 LeuValGlyGlnLeuL
22 AATATGTTTCTTTGATAGGTGGCAAGAAGACTTTCTTTAATAAAACATCCAGAGTGCTCC	ThrThrIleLysProGlyLeuAlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGln 133	Qy 114 ThrThrIleLysProc
11762 TTTCAATTTAITTTCCTTTGCATCTTTTCGTTTCACAGTATTTAATTTTAIGACTCTAAAA 11821 205AlaargargLeuSerLeuIleLysHisDroGluCysSer 217	ATAGTACAAGAAGCTCTTTCTGCCAGTGGAGTCTCTCCAAGTGACCTCTCAGCAATTGCA 10742 OV	Db 10683 ATAGTACAAGAAGCTC
04	a 113	94
11702 TATATTTGCCAAAGTATAGCATGTTTTATTCATTCAGGGGTTTTTTGTTTG	LYBING-LY-LY-LIPVALPTO-FOALAA-AGING-INLEGHIBARGG-HABRILLEGHIAIRG 93	Db 10623 AGAACAGGTGGGATTG
04		-10-649-273-
11642 TATTGTTCGGGTCATCATAAGGAACAGGTTGTCTGCTTACCTGAATATCAGCTATAGTC 11701		
204 204	Mismatches: 2 Indels: 657 - Qy	Best Local Similarity: 32.20% Query Match: 55.84%

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APPLICANT: Lagace, Robert, E.
APPLICANT: Patterson, Chandra
APPLICANT: Berg, Kim, L.
APPLICANT: Berg, Kim, L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF FILE REFERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT APPLICATION NUMBER: 00/140,121
PRIOR APPLICATION NUMBER: 00/140,121
PRIOR PILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS:
41
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   SOFTWARE:
SEQ ID NO 38
                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                               Sequence 38, Application Patent No. 6632636
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                   PERL Program
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; OTHER INFORMATION: Incyte template ID No. 6632636
; PUBLICATION INFORMATION:
US-09-596-002-38
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                                                                                    GlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHis 291
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Patent No. 6673910

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARTITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 806
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                                                                                                           ThrileLysProGlyLeuAlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeu 134
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                                  ValGlyGlnLeuLysLysProPheIleProIleHisHisMetGluAlaHisAlaLeuThr 154
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                                                                           ACCAAAGGCCCCGGGCTGATTGGGGGCATTGATGACAGGGGCATTATTTGGGCGGACGCTG
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LENGTH: 1206
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                                                                                                                          GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                               Sequence 801, Application US/09252991A Patent No. 6551795
                                                                       PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
ORGANISM: Pseudomonas aeruginosa
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CURRENT FILING DATE: 1999-02-18
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PRIOR ETLING DATE: 1998-02-18
PRIOR ETLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 884
LENGTH: 1059
TYPE: DNA
ORGANISM: Beeudomonas aeruginosa
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US-09-252-991A-884/c
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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139 LysLysProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThr 158
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                                                                                                                                                                                                                 ValProProAlaAlaGlnGlnLeuHisArgGluAsnIleGlnArgIleValGlnGluAla 98
                                                                                                                                                                                                                                                      GGCCTGCTGGCCGACGCGCTGTTCAGTCAGATCGACCTCCATCGCGTCTACGGCGCGTC
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                                                   GCCTGGTCGGCCTGCTGGTGGGGGGCTTCCTGTGCCCAGGCGATGGCCTTCGCCTGG
                                                                                GlyLeuAlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeu 138
                                                                                                                                                LeuSerAlaSerGlyValSerProSerAspLeuSerAlaIleAlaThrThrIleLysPro 118
                                                                                                                                                                                  GTGCCCGAGCTGGCCTCGCGCGACCACGTCAAGCGCATGCTGCCGCCTGATCCGCCAGGTG
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                                                                                                                           CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2341
                                                                                                                                                                                                                        Sequence 2341, Application US/09543681A

PATENT NO. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001
                                                                                              LENGTH: 1074
TYPE: DNA
                                                                               ORGANISM: Proteus mirabilis
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   Length:
Matches:
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                                                                                                                                   Asn---AlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAla 336
                                                                                                                                                                                                         ValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsn
                                                                                                                                                                                                                                                                                                                                                               ThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPhe
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                                                                              LeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeuCys
                                                                                                             GGCTTTAAACGCTTAGTGATGGCTGGGGGGGCGTAAGTGCTAACCGTACTTTACGCGCCCAAA 885
                                                                                                                                                                            GCAATAAAATGTCGTCGAGCA----
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                                                ATGGCGATGATAATGGAACAACTCGGAGGGGAAGTGTTTTATGCTCGCCCTGAGTTATGT
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; Sequence 6612, Application US/09902540
; Patent NO. 6833447
; GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Section and Comment of Current Application Number. US/09/902,540
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
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Best Local Similarity:
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PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 6612
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CTCGTCCTAGGACTGGAAACCTCGTGTGATGAGACTGCCGCCGCCGTCGTGGAGGACGGC
                                                                                                                                                                                                            LeuLysLysProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeu
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GCCGGCGAGGCATATGACAAGACCGCTCGCATCCTCGGCCTG---CCGTATCCG-----
                             ProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCys
                                                                                          LeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAla
                                                                                                                          ThrAsnLysVal---GluPheProPheLeuValLeuLeuIleSerGlyGlyHisCysLeu
                                                                                                                                                                                       ACGGGCAAGCCCTTCGTGGGCGCCAACCACCTGGAGGGCCACCTGCTGGCCATCCGGCTG
                                                                                                                                                                                                                                                   CCCGGACTCATCGGCGCCCCCTGCTGGGAGTGCAGGTGGCCAAGGGCTTGAGCCTGGCG
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                                                                                                                                                                                                                                                                                                                  GCGCTGACGCGGGCGAACAAGACGCTCGACGACGTGGACCTCATCGCCGTCACGTCCGGC
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                                                            CTCTACGAGGTGCÁGGCCTACGGGCAGTACCGGCTGGTGGGCAGCACGCGCGÁCGACGCG
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Matches:
Conservative:
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RESULT 12
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                                                      US-10-649-273-2 (1-414) x US-09-902-540-503 (1-2582)
                                                                                                    Query Match:
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                                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                   SEQ ID NO 503
LENGTH: 2582
TYPE: DNA
ORGANISM: Myxococcus xanthus
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                                                                                                                                                                                                                                                                                                                 APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
CURRENT FILING DATE: 2001-07-10
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                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
1525 CTCGTCCTAGGACTGGAAACCTCGTGTGAAGACTGCCGCCGCCGTCGTCGTGGAGGACGGC 1466
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Matches:
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US-08-087-797-1
Sequence 1, Application US/08087797 Patent No. 5543312 GENERAL INFORMATION:
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DB:
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1315 base pairs
TYPB: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,797
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Layton, Jr., Samuel G.
REGISTRATION NUMBER: 22807
REFERENCE/DOCKET NUMBER: 3374-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 704 377 1561
TELEPHONE: 704 377 1561
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HYPOTHETICAL: N
ANTI-SENSE: NO
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APPLICANT: Lo, Reggie Y.C.
APPLICANT: Abdullah, Khalid M.
TITLE OF INVENTION: Pasteurella Haemolytica
TITLE OF INVENTION: Glycoprotease
TITLE OF INVENTION: Gene and the Purified Enzyme
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CORRESPONDENCE ADDRESS:
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STATE: No. 5543312th Carolina
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                        gGluAsnIleGlnArgIleValGlnGluAlaLeuSerAlaSerGlyValSerProSerAs 108
                                                                              AATTGATATGCACGCCGATTACGGTGGCUTAGTCCCTGAACTGGCTTCTCGAGACCATAT 295
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3-09-557-884-1/c
3-09-557-884-1/c
Sequence 1, Application US/09557884
Sequence 1, Application US/09557884
Patent NO. 6506581
; GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of TITLE of INVENTION: The Haemophilus influenzae.)
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 CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tGluAlaHisAlaLeuThrIleArgLeu---ThrAsnLysValGluPheProPheLeuVa 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lAlaSerAsnPheTyrTleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysTh
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                553208 ATCTTAGGCATTGAAACTTCCTGTGATGAAACGGGCGTGGCGATTTATGATGAAGAAAAA 553149
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MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ
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GlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCysSer
                                                        GTGCGTGTCGATGGTGAAGAAAATATGAAGTGATAAGGAGAATCTATTGATGATGCTGCT
                                                                                                                               GACAATTCACCGCACTTTCCTTTTGTTGCTCTGTTGGTATCGGGTGGCCACACTCAATTA
                                                                                                                                                                                                                                                                                                            GlyLeuAlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeu 138
                                                                                                                                                                                                                                                                                                                                                                                                                      GTTCCTGAATTAGCATCACGTGATCATATTCGGAAAACAGCACCTCTTATTAAAGCGGCA
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                AATGTTCCTGCGATTGGTGTTCATCATATGGAAGGGCATTTACTTGCGCCAATGCTTGAT
                                                                                                                                                                                                                                                                          GGGCTTGTTGGCGCATTGCTTGTCGGTGCTACGATTGCACGTTCTTTAGCCTATGCTTGG
                                                                                           AlaLeuValGlnGlyValSerAspPheLeuLeuGlyLysSerLeuAspIleAlaPro
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Matches:
Conservative:
Mismatches:
Indels:
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MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOPTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSES: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
                                                APPLICATION NUMBER: 08/487,429
PILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
PILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                APPLICATION NUMBER: US/09/643,990A
PILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Robert D. Fleischmann
Mark D. Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF
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               NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGGCTATAAACGTTTAGTGATTGCGGGAGGGGTGAGCGCAAATAAAAAACTTCCGAGAA 552369
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REFERENCE/DOCKET NUMBER: PB186P1C1
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INVENTION: The Nucleotide sequence of
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The The Theorem
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TELEPAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.:
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 ValProProAlaAlaGlnGlnLeuHisArgGluAsnIleGlnArgIleValGlnGluAla
                                                                                                                                              AspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGln 257
||||:::
|||||||:::
ACATTTCCACGTCCAATGACAGATCGTGCAGGCCTTGATTTTAGTTTTTCTGGTTTAAAA 552570
                                                                                                                                                                                                                                                              ThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPhe
                                                                                                                                                                                                                                                                                                   GGCGAAGCCTTTGATAAAACAGCAAAATTACTTGGACTA---GATTATCCA-----
                                                                                                                                                                                                                                                                                                                                        GlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATGTTCCTGCGATTGGTGTTCATCATATGGAAGGGCATTTACTTGCGCCAATGCTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnValLeuGlyGluAlaIleHisSerGlnThrGluValHisLeuLysThrGlyGlyIle
                         GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys
                                                                        <u>ACATTTGCCCCCAAATACAGTTAATCAAGCAATTAAAAAACGAGGGCGAACTGATAGAGCAA</u>
                                                                                               HisValThrAspLysIleIleMetLysLysGluLysGluGluGly------IleGluLys 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysLysProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeu---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyLeuAlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeu 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuSerAlaSerGlyValSerProSerAspLeuSerAlaIleAlaThrThrIleLysPro 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTAGAGGAAGCCAATTTAACCGCGAGCGATATTGATGGTATTGCTTATACGAGTGGCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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475.50
50.74%
35.40%
22.38%
ACTAAAGCAGATATTGCTTATGCTTTCCAAGATGCGGTGGTGGAT 552465
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Matches:
Conservative:
Mismatches:
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Search completed: February 16, 2005, 21:50:50 Job time : 2493.15 secs

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-Q-/cgn2 1/USPTO_spool/USI0649273/runat_14022005 114706 16497/app_query.fasta_1.1429
-Q-/cgn2 1/USPTO_spool/USI0649273/runat_14022005 114706 16497/app_query.fasta_1.1429
-DB=Published_Applications_NA_QFMT=fastap_SUFFTX=rnpb_MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -RND=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10649273 @CGN 1 1 1053 @TUNAt 14022005 114706 16497
-NCPU=6 -LOUPL3 - NO_MANAP -LARGSQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPEON=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                                                                                                                n2_6/ptodata/2/pubpna/USO9A PUBCOMB.seq:*
gn2_6/ptodata/2/pubpna/USO9A PUBCOMB.seq:*
gn2_6/ptodata/2/pubpna/USO9B PUBCOMB.seq:*
gn2_6/ptodata/2/pubpna/USO99 NEW PUB.seq:*
gn2_6/ptodata/2/pubpna/USO0A PUBCOMB.seq:*
gn2_6/ptodata/2/pubpna/USO0A PUBCOMB.seq:*
gn2_6/ptodata/2/pubpna/USOOA PUBCOMB.seq:*
gn2_6/ptodata/2/pubpna/USOOA PUBCOMB.seq:*
gn2_6/ptodata/2/pubpna/USOA PUBCOMB.seq:*
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_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9 469 0 468 1 468 2 467.5 3 465.5 4 465.5 5 65	Sco	rit .
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Sequence 15870, A Sequence 3118, Ap Sequence 3119, Ap Sequence 21633, A Sequence 19220, A Sequence 29584, A Sequence 31809, A Sequence 31809, A	scription	

4.1

## ALIGNMENTS

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Sequence 1, Application US/10067443

Publication No. US20030082782A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER: OF SEQ ID NO.1
SEQ ID NO.1
LENGTH: 2197
TYPB: DNA
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ORGANISM: Homo

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                         AspLysIleIleMetLysLysGluLysGluGluGlyIleGluLysGlyGlnIleLeuSer 280
                                                                           ProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThr 260
                                                                                                                                                                                              LeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCysSerThrMetSer
                                                                                                                                                                                                                                                                                                                                                   ProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAsnLys
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SerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArg 300
                                                                                                                                                                               CTTGACAAGGTGGCAAGAAGTTTCTTTAATAAAACATCCAGAGTGCTCCACCATGAGT
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (231)..(1472)
US-10-649-273-1
                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 CNT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/087,443
PRIOR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10649273 Publication No. US20040043407A1 GENERAL INFORMATION:
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (231)..(1472)
US-10-651-722-1
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Publication No. US20040048302A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITILE OF INVENTION: POLYNUCLECTIDE ENCODING A N
FILE REFERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722

CURRENT FILING DATE: 2003-08-29

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR APPLICATION NUMBER: US 10/067,443

PRIOR FILING DATE: 2002-02-05

PRIOR PILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 71

SOPTWARE: PatentIn version 3.2

INVERT. PATENTION IN THE PATENTIAL OF SEQ ID NO 1

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                                                        ProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAsnLys
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Sequence 21, Application US/10067443

Publication No. US20030082782A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITILE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED I
ITILE OF INVENTION: SPINAL CORD, MP-1

FILE REFERENCE: DO073 NP
CURRENT APPLICATION NUMBER: US/10/067,443

CURRENT FILING DATE: 2002-02-05

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR FILING DATE: 2001-02-05

PRIOR FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin version 3.0

SEQ ID NO 21

LENGTH: 1387

TYPE: DNA

ORGANISM: homo sapiens

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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A
FILE REFERENCE: D0073 CNT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR PILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER: D850 ID NOS: 71
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SEQ ID NO 21
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TYPE: DNA
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 LeuGlyGluAlaIleHisSerGlnThrGluValHisLeuLysThrGlyGlyIleValPro
                                                 GlyIleGluThrSerCyeAspAspThrAlaAlaAlaValValAspGluThrGlyAsnVal
                                                                                            GAATTTTTAAGAAGTTTTAATTTTCATCCTGAAACACTATTTCTTCATAAAATAGTATTG
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GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp 395
                                                                                                                                                          AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu 355
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                                                                                                        TGCACTGATAATGGCATTATGATTGCATGGAATGGTATTGAAAGACTACGTGGTGGCTTG 1223
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RESULT 6
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Publication No. US20040048302A1
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Best Local Similarity:
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CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
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LENGTH: 1387
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
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Sequence 6, Application US/10012140

Publication No. US20030090017A1

GENERAL INFORMATION:
APPLICANT: Leiby, Kevin R.
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
ITILE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
ITILE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND CURRENT APPLICATION NUMBER: US/10/012,140

CURRENT APPLICATION NUMBER: US/10/012,140

CURRENT PILING DATE: 2001-11-08

PRIOR APPLICATION NUMBER: 60/246,768

PRIOR APPLICATION NUMBER: 60/246,772

PRIOR APPLICATION NUMBER: 60/246,772

PRIOR PILING DATE: 2000-11-08

PRIOR PILING DATE: 2000-11-08

PRIOR PILING DATE: 2000-11-18

PRIOR PILING DATE: 2000-11-18

PRIOR PILING DATE: 2000-11-18

PRIOR PILING DATE: 2000-11-15

NUMBER OF SEQ ID NOS: 49

SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-012-140-6
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Sequence 4, Application US/10012140

| Publication No. US20030009017A1
| GENERAL INFORMATION:
| APPLICANT: Leiby, Kevin R.
| APPLICANT: Leiby, Kevin R.
| APPLICANT: Glucksmann, Maria A.
| TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
| TITLE OF INVENTION: THEREOF
| FILE REFERENCE: 381552004900
| CURRENT APPLICATION NUMBER: US/10/012,140
| CURRENT APPLICATION NUMBER: 60/246,768
| PRIOR APPLICATION NUMBER: 60/246,768
| PRIOR APPLICATION NUMBER: 60/246,772
| PRIOR FILING DATE: 2000-11-08
| PRIOR PILING DATE: 2000-11-08
| PRIOR APPLICATION NUMBER: 60/246,772
| PRIOR FILING DATE: 2000-11-15
| NUMBER OF SEQ ID NOS: 49
| SOPTWARE: PRASTSEQ for Windows Version 4.0
                                                                                                                                                                            LENGTH: 1820

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (146)...(1390)
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(1820)
OTHER INFORMATION: n = A,T,C or
US-10-012-140-4
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Best Local Similarity:
Query Match:
DB:
US-10-649-273-2 (1-414) x US-10-012-140-4 (1-1820)
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APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA; MOTOYUKI
APPLICANT: NACHARI, KENJI
APPLICANT: NACHARI, KENJI
APPLICANT: NASUHO, YASUHIKO
TITLE OP INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOPTWARE: Patentin Ver. 2.1
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LENGTH: 2208
TYPE: DNA
ORGANISM: Homo sapiens
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OTSUKA, KAORU
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IRIE, RYOTARO
TAMECHIKA, ICHI
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
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YAMAMOTO, JUN-ICHI
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RESULT 10
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GENERAL INFORMATION:

APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.

APPLICANT: Gloriburg, Wendy M.

APPLICANT: Zlotnik, Albert

TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

FILE REFERENCE: 05882.0193.NPUS01

CURRENT APPLICATION NUMBER: US/10/723,860

CURRENT FILING DATE: 2003-11-26

PRIOR APPLICATION NUMBER: 60/429,739

PRIOR FILLING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 8393

SOFTWARE: PatentIn version 3.2

SEQ ID NO 7447

LENGTH: 2890

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (646)...(657)
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Best Local Similarity:
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OTHER INFORMATION: n i
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APPLICANT: TANG, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Men, Felyan
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
TITLE OF INVENTION: No. US20030219745A1el Nucleic Aci
TITLE OF INVENTION: NUMBER: US/10/120,988
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 09/774,528
PRIOR APPLICATION N
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Publication No. US20030082782A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REPERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/262,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PRILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.0
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TYPE: DNA
ORGANISM: homo sapiens
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                   ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe 307
                                                                           GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla
                                                                                                                                     AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys
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LENGTH: 1526
TYPE: DNA
ORGANISM: homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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US-10-649-273-2 (1-414) x US-10-649-273-23 (1-1526)
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CTTTTGATTTCTGGAGGTCACTGTCTGTTTGGCATTAGTTCAAGGAGTTTCAGATTTTCTG
                                                                                             ATGGAGGCTCATGCACTTACTATTAGGTTGACCAATAAAGTAGAATTTCCTTTTTTAGTT
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-651-722-23
; Sequence 23, Application US/10651722
; Publication No. US20040048302A1
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                                                                                                                                                                                SEQ ID NO 23
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE,
FILE REPERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
NUMBER OF SEQ ID NOS: 71
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TYPE: DNA
ORGANISM: homo sapiens
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Sequence 20, Application US/10067443
Publication No. US20030082782A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITILE OF INVENTION: POLYNUCLECTIDE ENCODING A 1
FILE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
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12422 CCATTTCTTGTACTAGTTGGTAGCTTTATGGGACAGCTGTATAGCTTCTATGGCACATA	Db 11342 ATATACATTAACATTAAAGATGCAATGCAATGAGAATTAAATCACACAATTACT 11401
321	Qy 204 204
12362 CITTATIGCTTATIGCTAGECCTIGACAGTATIGAAATTATIGCAGGATAGGAAAGACTAACAG	Db 11282 ATGTGAAAGAACGTGCTTCGTAAACTAACATACTGCAAAAAAGGTAAAATAAGAGAATAT 11341
321	Оу 204 204
12302 CACTTYGCAATATGTTACTTTTTTCCCAAGACCTTGACCTTGTGTTTAGGATGAACAGAT	Db 11222 ATCTGTACATAAAGGCTGAAATAGTTTGCCAGATACAGTTATGTATTTTGCCCAAATAATGT 11281
321	Оу 204 204
	Db 11162 AAGAGTAGTACACAATTTTATAATTCTTAGCCTTTCTTAATAAAATGGTAAGAGGTTCAT 11221
312 pLeuLeuProGlnAsnAsnAlaValLeu	Оу 204 204
	11102 TATTTCTGAATTTTATCTTAGTAAACTGAAAAAAATTCACATATGGTGAGAAAAAATAGA
292 rMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAs	
12122 TATTGÁGAÁGGGGCÁÁATCCTGTCTTCÁGCÁGCÁGACÁTTGCTGCCÁCÁGTÁCÁGCÁCÁC	11042 TTTGTTATGTTGTCCATTTCAACTAAGTAGCAATAGATGTGCTACCACCATTCACCTAAA 1
272 yIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisTh	204
12062 AAAGTTGAACAGATAAATATTCCTGGATTGTGCCTAAAAATAGCTGCTCATTTCTGCAG	
272	eAlaProGlyAspMetLeuAspLysVal
	Qy 174 HisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuGlyLysSerLeu 193
11942 ĠACATCAAAACCTCCCTTGCCATCATGCTAAAAATTGTGGATTTTTCTTTTTACTGGACTTCAA	10863 ACTATTAGGTTGACCAATAAAGTAGAATTTCCTTTTTAGTTCTTTTGATTTCTGGAGGT 1
238 AspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGln	154 ThrIleArgLeuThrAsnLvsValGluPheDroPheLeuValLeuLeuTleSerGlvGlv
11882 ACCATGAGTGGTAGAAACCATAGAACATTTGGCCAAACAAGGAAATAGATTTCATTTT	Qy 134 LeuValGlyGlnLeuLysLysProPheIleProIleHisHisMetGluAlaHisAlaLeu 153
218	10802
205	Qy 114 ThrThrIleLysProGlyLeuAlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGln 133
11762 TTTCAATTTATTTCCTTTGCATCTTTTCGTTTCACAGTATTTAATTTTATGACTCTAAAA	10683 ATAGTACAAGAAGCTCTTTCTGCCAGTGGAGTCTCTCCAAGTGACCTCTCAGCAATTGCA
204	94 IleValGinGluAlaLeuSerAlaSerGlvValSerProSerAspLeuSerAlaIleAla 113
11702 TATATTTGCCAAAGTATAGCATGTTTTATTCATTCAGGGGTTTTTTTT	106
204	74 Evenhadiveloristenski store to the teachers of the teachers
11642 TATTGTTCGGGTCATCATAAGGAACAGGGTTGTCTGCTTACCTGAATATCAGCTATAGTC	649-273-2 (1-414) x US-10-067-443-20 (1-14364)
204	Match: 55.84%
11582 TCAAGCCCATTTTCCAACCAATAGAAGAGCAAACATAGACAGGGGCAGTGATTGGCCTCT	t Similarity: 32.30% Conservative:
204	. 7.32e-132 Length: 1186 SO Matches.
11522 TAGGAAGTATAGGACAAGTTCTTATTATTGACGTTCATCATTAAGCAGTTATTGTCAACT	Alignment Scores:
204	; ORGANISM: homo sapiens Qy
11462 GCCATATATAGGAAAACAAACAAACAAACAAACAAACACTGCTTCCCCACAGTGAAATAA	; TYPE: DNA
204	SOPTMARE: PatentIn version 3.0
11402 TACACCACAGACAGGGTCCCCCCCCCCCCCTTTGTTTTAGAATACTACAGAGGCTACT 11461	; PRIOR FILING DATE: 2001-04-10 Db

leGluGlyIleArgTyrGluProLys 389 	79 isAspI	Qy 3	
TITAATGCTTCTTAGTTAGGAATGGTATTGAAAGACTACGTGCTGGCTTGGGCATTTTAC 13501	442 TTTAATGCTT	Оу Db 134	
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  CATTATGATTGCATGGTAAGCCACAGGATATACGTGCTTCACTCATAACTATGTAAATAT 13381	322 CATTATGATT	Db 13:	н
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uThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGl 360	340 uThrAsnAla           262 AACAAACGCA	Оу 133	н ^
SCATCTGGTGGTGTCGCAAGTAACTTCTATATCCGCAGAGCTCTGGAAATTTT 13261	202 TCAGGTTGCA	13	
ValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLe 340	322ValAla	φ	_
TTTAATTAGCAGCTTGGTTCATATCCATATATGATAGTTATTTTGGTTTTCTCAATTCCT 13201	142 TTTAATTAGC	Db 131	н
321	321	γ	_
CCATCTCAAAATGGGATAGTTTATTATTGTTTAATGCTGATATTTTTTCTCCAGG 13141	082 CATTACCCAT	Db 13(	н
321	321	2 YQ	_
ATTAGTAATTTTTTTCTTTCCAAATTTTTATTACATAGATATGTCATCTGCC 13081	022 TTAGAATTAT	Db 13(	н
321	321	γ	_
AATATTTAGATGAAAGGTTGGAAGAAAATATACAAAAATGCTAGTAATGTTTGTATGCTA 13021	962 AATATTTAGA	Db 129	-
321	321	Qy :	_
AATAAAAATTTCAGGGTCTAAAATAGTGTACTATGATTGAAATTATATTAAATA 12961	902 САЛАЛТАЛТА	Db 129	н
321	321	Qy	_
NTTTTACATGGATATCAAAGAATAATTTTTTCAGAGTTATGTAGTAAAATGCA 12901	842 AGATGGAATT	Db 128	н
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321	321	Qy .:	_
GTTTGTTTGTTTTTTAATAAGCCAGTCAAATTTAGCAGTGGGAGGTGGTAT 12661	602 ATCCCTTTGT	Db 126	н
321	321	<b>Q</b>	_
TGCTATCACTATTTTTAGAAAAATAGGTGGATTTCCTTCATCCTTTGATGAA 12601	542 GCAGTAACTG	Db 125	п
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Search completed: February 17, 2005, 01:26:44 Job time : 878 secs

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H71545
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B86515
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A;Residues: 1 387 <AND>
A;Cross-references: UNIFF
A;Experimental source: st
C;Genetics:
A;Gene: gcp; RP037
C;Superfamily: O-sialogly
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Nature 396, 133-140, 1998
A;Fitle: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Fitle: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Recession: E7171
A;Accession: E7171
A;Accession:
A;Title: The Genome of the Natural Genetic A;Reference number: AB2577; MUID:21608550; A;Accession: AB2902 A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                    Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A; Authors: Yoo, H.; Tao, Y.; Biddle,
                                                                                                                                                                                                                                                                      C;Accession: AB2902
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, I
                                                                                                                                                                                                                                                                                                                                                                     O-sialoglycoprotein endopeptidase gcp [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: D97677
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-366 < KUR>
A;Cross-references: GB:AE007869; PIDN:AAK88373.1; PID:g15157858; GSPDB:GN00169
C;Genetics: GB:C4806
A;Map position: clicular chromosome
C;Superfamily: O-sialoglycoprotein endopeptidase
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A;Cross-references: GB:AE008688; PIDN:AAL43632.1; PID:g17741154; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
C;Genetics:
A;Gene: gcp
A;Map position: circular chromosome
C;Superfamily: O-sialoglycoprotein endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quro. A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable o-sialoglycoprotein endopeptidase (glycoproteinase) [imported] - A. C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: D97677
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                                                                                                                                            137;
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      95
                                                                         39 VLGIETSCDDTAAAVV----DETGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 VLGIETSCDDTAAAVV----DETGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRI
    VQEALSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALT 154
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                                                  ILGIETSCDETAASIVVRHADGRGEIVSDVVLSQLEEHSAYGGVVPEIAARAHVEALDTL
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                                                                                                                                       58;
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                                                                                                                                         Mismatches 142;
                                                                                                                                                                                Length 366;
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ppas, C.;
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Markelz,
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ckelz, B.;
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VEEALDQAGVKLADVDATAATSGPGLIGGLLVGLMTGKAIAKAAGKPLYAINHLEGHALT

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O-sialoglycoprotein endopeptidase (EC 3.4.24.57) [imported] - Rickettsia conorii (Stra C. Species: Rickettsia conorii (C. Species: Rickettsia conorii (C. Species: Rickettsia conorii (C. Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001 C. Accession: B97707 R. Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Science 293, 2093-2098, 2001 A.; Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A. Reference number: A97700; MUID:21442074; PMID:11557893 A.; Accession: B97707 A.; Status: preliminary A.; Status: preliminary A.; Status: preliminary A.; Fournier (C. Superfemily: O-sialoglycoprotein endopeptidase C.; Superfemily: O-sialoglycoprotein endopeptidase C.; Keywords: hydrolase; metalloproteinase
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les 125; Conservative
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:||GIESSCDDTAVSIITENRBILSNIIISQNTEHAVFGGVVPBIAARSHLSHLDKALKNV 63
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                                                                                                      LEILTNATQCTLLCPPPRLCTDNGIMIAWNGIER 370
                                                                                                                                                                                                                                                                               MSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK-KEKEEGIEKGQ
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                                                                               LSSCAKTYGYRLIYPPIHLCTDNAAMIAYAGLER 320
                                                                                                                                                              ----INDIAASFQFTIGEILSSKVQDAIRAYEQITNNFDKKN--IVIAGGVAANKYLQKI 286
                                                                                                                                                                                                  ILSSAADIAATVOHTMACHLVKRTHRAILFCKO-RDLLPQNNAVLVASGGVASNFYIRRA 336
                                                                                                                                                                                                                                             FPGGPEIEKRAKLGDPHKYKFPKPIINSGNCNMSFSGLKTAVRTLIMTLKEINDTV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 540.5; DB 2;
Pred. No. 4.9e-36;
58; Mismatches 132;
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O-sialoglycoprotein endopeptidase (EC 3.4.24.57) [imported] - Brucella melitensis (strair C.Species: Brucella melitensis
C.Species: Brucella melitensis
C.Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C.Accession: AB3274
R.DelVecchio, V.G., Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A.Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi A.Reference number: AD3252; PMID:11756688
A.Recession: AB3274
A.Recession: AB3274
A.Recession: AB3274
                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-367 <STO>
A;Cross-references: GB:AE005673; NID:g13421168;
                                                                                                                                                                                                                                                                                                                                        R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Bisen, J.; Heidelberg, J.I. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolona n, J.; Brmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptidase M22 family protein [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001 C;Accession: F87257
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C;Superfamily: O-sialoglycoprotein endopeptidase
C;Keywords: hydrolase; metalloproteinase
                                                                                                                                                                                                                                                                                   A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE008917; PIDN:AAL51357.1; PID:g17982056; GSPDB:GN00190 A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-359 <KUR>
                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 132;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 VLGIETSCDDTAAAVVDE----TGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 VQEALSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQ-NNAVLVASGGVA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARLTDGLPFPYLLLLVSGGHTQMVLVRGIGDYERLGTTIDDALGEAFDKTAKLLGL-PYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRLTNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDRALNDAGLKLYEVDAVAATAGPGLIGGLIVGLMTAKALAMAAQKPFYAVNHLEGHALT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIGIETSCDETAAAIVERDDMGEGRILSNVVLSQIAEHEPYGGVVPEIAARAHVEALDRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNFYIRRALBILTNATQCTLLCPPPRLCTDNGIMIAWNGIER 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGL----QHVTDKIIMKKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANKTLRAALENLCTRHGFAFIAPPLNLCTDNAAMIAWAGAER
                                                                                  O-sialoglycoprotein endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GGPAVERMALQGDQKRFALPRPLKGEARLDFSFSGLKTAVRQTATELVPLTDQ-
25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.4%; Score 539.5; DB 2; 38.6%; Pred. No. 6.3e-36; tive 52; Mismatches 127;
Score 535.5; DB 2; Pred. No. 1.4e-35;
                                                                                                                                                                        PIDN: AAK22058.1; GSPDB:GN00148
                          Length
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Best Local Similarity

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A;Reference number: Z19027
A;Reference number: Z19027
A;Roession: T18825
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-421 <WIL>
A;Residues: 1-421 <WIL>
A;Cross-references: EMBL:Z81030; PIDN:CAB02716.1; GSPDB:GN00023; CESP:C01G10.10
A;Experimental source: clone C01G10
C;Genetics:
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R;Matthews, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Introns: 31/2; 72/3; 122/2; 177/1; 272/3; 315/1; 353/2;Superfamily: O-sialoglycoprotein endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                     -NKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECS
                                                                                                                                                                                                                                                                                                                                   LSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRLT 158
                                                                                                                                                                                                                                                                                                                                                                                                              VLGIETSCDDTAAAVVDETGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRALBILTNATQCTLLCPPPRLCTDNGIMIAWNGIBRLRAGLGILHDIEGIRYEPKCPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SARLGADIAYPFILLLVSGGHCQLLEVSGVGACKRLGTTIDDAAGEAFDKIAKSLGL-PY
  RALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIBRLRAGLGILHDIEGIRYBP-----
                                                                                                                             GIHVGAAVEILASRASADGHLRYPIFLPNVPKANMNFDQIKGSYLNLLERLRKNSETSID
                                                                                                                                                                   TMSGGKAIEHLAKQGN---RFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIE
                                                                                                                                                                                                                                                                                              LNDAGTSPKDLDAVAVTVTPGLVIALKEGISAAIGFAKKHRLPLIPVHHMRAHALSILLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAALLADCEKNGFSFAAPPLAYCTDNAAMIALAGAERL--ALGIFDDLDAIA-RPRWPL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYI 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PECSTMSGGKAI EHLAKQGNRFHFDI KPPLHHAKNCDFSFTGLQHVTDKI IMKKEKEEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAAEAVRAAGVGFGDLDGVAATAGPGLVGGVMVGLAFGKAVALARGAPLVAVNHLEGHAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVQEALSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHAL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LILGLETSCDETAASVVRRAADGTVTVLSSVIGTQFEKHAPFGGVVPEIAARAHVESIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVLGIETSCDDTAAAVV----DETGNVLGBAIHSQTEVHLKTGGIVPPAAQQLHRENIQR
                                                                                    KGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIR 334
                                                                                                                                                                                                                                                                                                                                                                              VLGIETSCDDTAVAIVNEKREILSSERYTERAIQRQQGGINPSVCALQHRENLPRLIEKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                           --IPDFCASLONTVARHISSKLHIFFESLSEQEKLPKQ---LVIGGGVAANQYIF 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -ARRDLAAGVQAAIARQLSERVDRAMKLYK--DSHDPEDLRFVVAGGVAANGAV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.7%; Score 524; DB 2; Length 421; 33.4%; Pred. No. 1.4e-34; vative 77; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
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                                                                                                                             263
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A;Reference number: A82950; A;Accession: H83572 A;Status: preliminary R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A; Title: Complete genome sequence of Pseudomonas aeruginosa A; Reference number: A82950; MUID: 20437337; PMID: 10984043

PA01, an

opportunistic pathog

Hickey, Larbig,

M.J.; Bri K.; Lim, (strain

PAOI

C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

O-sialoglycoprotein endopeptidase PA0580 [imported] - Pseudomonas aeruginosa

C; Accession: H83572

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RESULT
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C;Superfamily: O-sialoglycoprotein endopeptidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sialoglycoproteinase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: G70369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-335 < AQF >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 24.3%; Score 516.5; DB 2; Best Local Similarity 36.5%; Pred. No. 4.2e-34; Matches 130; Conservative 66; Mismatches 125;
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---EDIAYSFQETVVEILLEKS----LWAMKKTGIKR----LVVVGGVSANSRLR----EV
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                                                                                                                              SSAADIAATVOHTMACHLVKRTHRAILFCKORDLLPONNAVLVASGGVASNFYIRRALEI 339
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A;Title: Complete genome sequence of enterohemorrhagic Bscherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C91122
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-337 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37370.1; PID:gl3363420; GSPDB:GN00154
A;Cross-references: strain O157:H7, substrain RIMD 0509952
C;Gene: EC83947
C;Superfamily: O-sialoglycoprotein endopeptidase
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A;Cross-references: GB:AE004494; GB:AE004091; NII
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: gcp; PA0580
C;Superfamily: O-sialoglycoprotein endopeptidase
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                                                                                                                                                                                                                                                                                                                      VLGIETSCDDTAAAVVDETGNVLGBAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQBA 98
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                                                                                                                                                                                                                                                                                                                                                                                             23.0%; Score 488.5; DB 2; 35.2%; Pred. No. 7.8e-32; ative 55; Mismatches 148;
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O-sialoglycoprotein endopeptidase (BC 3.4.24.57) - Escherichia coli (strain C;Species: Escherichia coli (c;Species: Bscherichia coli (c;Date: 30-Jun-1988 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004 C;Accession: F65934; D2304; P2304; P2304; P3304; P3304; P4304; P4
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A;Molecule type: DNA
A;Residues: 1-337 <STO>
A;Cross-references: GB:AE005174; NID:g12517643; PIDN:AAG58198.1; GSPDB:GN00145; UWGP:Z44J
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; liller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamon Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85967
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C;Superfamily: O-sialoglycoprotein endopeptidase
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DNPPEPPEVALLVSGGHTQLISVTGIGQYELLGESIDDAAGEAPDKTAKLLGL-DYP----
                                                                                                                                                                                                                                                                                                                                                  TNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECS
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                                                                                                                                                           ILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRAL
                                                                                                                                                                                                                                                                     TMSGGKAI EHLAKQGNRFHFDI KPPLHHAKNCDFSFTGLQHVTDKI IMKKEKEEGI EKGQ
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                                                                                                         --QTRADIARAFEDAVVDTLMIKCKRAL-----DLTGFKR--LVMAGGVSANRTLRAKL
                                                                                                                                                                                                                   ---GGPLLSKMAAQGTAGREVFPRPMTDRPGLDFSFSGLKTFAANTI----RDNGTDD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLGIETSCDETGIAIYDDBKGLLANQLYSQVKLHADYGGVVPELASRDHVRKTVPLIQAA
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Burland, V.; Riley,

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K-12)

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Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant:
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AG0892
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-337 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07733.1; PID:g16504285
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F65094
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-337 <BLAT'
A;Cross-references: UNIPROT:P05852; GB:AE000388; GB:U00096; NID:g1789441; PIDN:AAC76100.
A;Experimental source: strain K-12, substrain MG1655
R;Nesin, M.; Lupski, J.R.; Svec, P.; Godson, G.N.
Gene 51, 149-161, 1987
A;Title: Possible new genes as revealed by molecular analysis of a 5-kb Escherichia coli
A;Reference number: A91573; MUID:87248073; PMID:3297921
A;Accession: D29049
A;Accession: D29049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: ygjD
A;Men position: 67 min
A;Map position: 67 min
C;Superfamily: O-sialoglycoprotein endopeptidase
C;Keywords: hydrolase; metalloproteinase; zinc
F;111,115/Binding site: zinc (His) #status predicted
                                                                                                                                                                                                                                                                                                                                  probable glycoprotease [imported] - Salmonella enterica subsp. enterica serovar T (;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AG0892 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Ch th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.;
A;Gene: STY3387
C;Superfamily: O-sialoglycoprotein endopeptidase
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A;Cross-references: GB:M16194; GB:X00773;
C;Genetics:
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Best Local
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                                                                                GSPDB:GN00176
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R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Recession: A10079

A;Recession: A10079
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C;Superfamily: O-sialoglycoprotein endopeptidase
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C;Species: Yersinia pestis
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A; Residues: 1-337 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
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Matches 123
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Best Local Similarity
Matches 123; Conserv
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 179
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                                                                           ENAPEFPFVALLVSGGHTQLISVTGIGEYLLLGESVDDAAGEAFDKTAKLLGL-DYP---
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                                   TMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQ
                                                                                                                                                        LKEANLSAKDIDAVAYTAGPGLVGALLVGATIGRALAFAWGVPAVPVHHMEGHLLAPMLE
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-GGPMLSRMAQQGTVGRFTFPRPMTDRPGLDFSFSGLKTFAANTIRANGDDD-----
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Search Job ti	Ъ	Q ,	뮹
Search completed: February 16, 2005, 13:09:20 Job time : 19.9 secs	279 LADMMQKRGGEVFYARPEFCTDNGAMIAYAGMVRLRSNLNSELSVSVRFRWPL 331	337 LEILTNATOCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPL 392	230QTRADIARAFEDAVVDTLAIKSKRALDQTGFKRLVIAGGVSANQTLRLK 278

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-MODEL-frame+ p2n.model -DEV=xlh
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Ygapop 10.0 , Ygapext
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## ALIGNMENTS

REFERENCE 2 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes MEDLINE 20499374 PUBMED 11042159 REFERENCE 1
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JOURNAL REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepare mouse tissues.
Please visit our web site for fur
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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Encyclopedia Project of Genome Exploration Research Group in
Genomic Sciences Center and Genome Science Laboratory in RIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Physical and Chemical Research (RIKEN), Laboratory for General Exploration Research Group, RIKEN Genomic Sciences Center RIKEN Yokohama Institute; 1-7-22 Seniero-Cho, Tsurumi-ku, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax.81-45-503-9216)
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6 (bases 1 to 2284)
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                 /codon_start=1
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/proteIn_id="BAC32450.1"
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VEFPPLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECST
                                                                                                                                                                                   /note="unnamed protein product; putative similar to PUTATIVE SIALOGLYCOPROTEASE TYPE 2 sapiens) (SPTR|Q9H4B0, evidence: FASTY, 80%ID,
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/clone_lib="RIKEN_full-length_enric
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221 - 145c
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                                                                                                                                                                                             Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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Meth. Enzymol. :
99279253
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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1622 bp mRNA linear HTC 03-APR-2004 Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610001M19 product:similar to PUTATIVE CIVIC CONTRACTOR CONTRACTO
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        FANTOM Consortium.
                                          The RIKEN Genome Exploration Research Group Phase
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Analysis of the mouse transcriptome based on of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1622)
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                                                                                                                                                                                         /codon_start=1
/protein_id="B827506.1"
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MSGGKAIBQLAKDGNRFHFTINPPMQNAKNCDFSFTGLQHITDKLITHKEKEEGIEKE
QILSSAADIAAAVGHATACHLAKRTHRAILFCKOKNLLSPANAVLVVSGGVASNLYIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="unnamed protein product; putative similar to PUTATIVE SIALOGLYCOPROTEASE TYPE 2 sapiens] (SPTR|Q9H4B0, evidence: FASTY, 80%ID,
                                                                                                                              GVDISREVAEAAIKVPRLKMAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     match=1242)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="whole body"
/clone_lib="RIKEN full-length enriched mouse
/dev_stage="10 days embryo"
207 1/61
                                                                                                                                                                        <u>KALBI VANATQCTTLLCPPPRLCTUNGIMI AWNG I ERLRAGLGVLHDVBD I RYBPKCPL</u>
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/db_xref="taxon:10090"
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                                                        AspLysIleIleMetLysLysGluLysGluGluGlyIleGluLysGlyGlnIleLeuSer
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Mus musculus O-sialoglycoprotein
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RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Parmer, A.A., Rubin, G.M., Hsieh, F., Diatchenko, L., Marusina, K., Parmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R. W., Touchman, J. W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                         Submitted (20-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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FEATURES

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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton,
Madan, Stephanie Rodrigues, Amy Sanchez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Institute for Systems http://www.systemsbiology.org
| 1GlnGlyValSerAspPheLeuLeuCeuGlyLysSerLeuAspIleAlaProGlyAspMe 200
                                                                                                                                                        sProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAsnLy
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/clone_lib="Soares_thymus_2NbMT"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="IMAGE:1226118"
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               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NGC Clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13342 row: 1 column: 21
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AGENCOURT 7790948 NIH_MGC_72 Homo
5', mRNA sequence.
BO42165
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 870)
11 (hases 1 to 870)
11 H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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BQ423651.1 GI:21118966
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              PheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCys
                                                                     ArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsn
                                                                                                              CACACAATGGCATGTCATCTTGTGAAAAGAACACATCGGGCTATTCTGTTTTTGTAAGCAG
                                                                                                                                                                    GAAGGTATTGAGAAGGGGCAAATCCTGTCTTCAGCAGCAGACATTGCTGCCACAGTACAG
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TTCTATATCCGCAGAGCTCTGGAAATTTTAACAAACGCAACACAGTGCACTTTGGTGTGT
                                                       AGAGACTTGTTACCTCAAAATAATGCAGTACTGGTTGCATCTGGTGGTGTCGCAAGTAAC
                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="melanotic melanoma"
/lab_host="pH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/clone="Torgan: skin; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Torgan: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Sycrage insert size 2 kb. Library constructed by Life
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/db_xref="taxon:9606"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                       Percent Similarity:
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                                                                                                                                                                                                                                                                                                Pred. No.:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 852)

Li (W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

AL Unpublished (2001)

On May 13, 2003 this sequence version replaced gi:30611736.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Emmail: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSDRT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAIO35ZEO7_CSO3317_1&c=1240.r
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sPro-LeuGlyValAspIleSerLys 398
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                                                                                                                                                                                                                                                                                                                                                                              /cell type="HELA CELLS COT 25-NORMALIZED"
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/clone lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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/clone="CS0DK001YE02"
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/mol_type="mRNA"
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                                                                                                                                                                                          2.41e-141
1353.50
96.14%
96.14%
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 922)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                 Homo sapiens (human)
Homo sapiens
                                                                                                                                   BQ961028
BQ961028.1 GI:22376506
                                                                                                                                                  AGENCOURT_8863711 NIH_MGC_18 Homo sapiens cDNA clone 5', mana sequence.
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                                                                                                                                                                     IMAGE: 6423902
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Best Local Similarity:
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High quality sequence stop: 584.
Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
eLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisVa
                                                                                              MetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCys-SerThrMe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 18"
/clone lib="NIH MGC 18"
/clone lib="NIH MGC 18"
/clone lib="NIH MGC 18"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI, cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:6423902"
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/db_xref="taxon:9606"
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91.80%
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RESULT 7
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1 (bases 1 to 701)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
plate: LLCM814 row: n column: 09
High quality sequence stop: 701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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                                          /tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone libe"NNH MGC 9"
/clone libe"NNH MGC 9"
/clone libe"NNH MGC 9"
/cloned into BcoRI/NDI Sites using the following 5'
adaptor: GGCACCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bdlg. 200 Rm2A BARC-East, Beltsville, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: tads@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt " -trim_fasta. Vector identified
by cross match using options -minmatch 12 -minscore 18
plate: 45 row: M column: 02
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Fax: 3015048414
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                  LeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeu 188
                                                                                      GluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuValLeu 168
                                                                                                                                                               SerPheSerLeuGlnLeuValGlyGlnLeuLysLysProPheIleProIleHisHisMet 148
                                                                                                                                                                                                                                                                                       GAAAATATTCAACGCATAGTACAAGAAGCTCTCTCTGCCAGTGAAGTCTCTCCAAGTGAA 180
                                                                                                                                                                                                                                                                                                           GluAsnIleGlnArgIleValGlnGluAlaLeuSerAlaSerGlyValSerProSerAsp 108
                                                                                                                                                                                                                                                                                                                                                           ACTGAAGTTCATTTAAAAACAGGTGGGATTATTCCTCCAGTAGCTCAACAGCTTCATAGA
                                                                                                                                                                                                                                                                                                                                                                                   ThrGluValHisLeuLysThrGlyGlyIleValProProAlaAlaGlnGlnLeuHisArg
                                                                                                                                                                                                                                                                                                                                                                                                                                TCGTTTAGCTTACAACTGGTAGACCAGTTTAAAAAGCCCTTCATTCCCATTCATCACATG
                                                                                                                                                                                                                                     LeuSerAlaIleAlaThrThrIleLysProGlyLeuAlaLeuSerLeuGlyValGlyLeu 128
TTGATTTCTGGAGGTCATTGTCTTTTGGCATTAGTTAGAGGAGTTTCAGATTTTCTTCTT
                                                                      GAGGCTCATGCACTCACTATTAGGTTAACAAATAAGGTAGAATTTCCGTTTTTAGTTCTT
                                                                                                                                                                                                                 CTCTCAGCAGTTGCAACCACCATAAAGCCAGGACTTGCTTTAAGCTTGGGCGTAGGTTTA
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Location/Qualifiers
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/lab_host="PH10B Tl phage resistant"
/clone_lib="BARC 9BOV"
/note="Organ: Abomasum; Vector: phgen-1; Site_1: EcoRV;
Site_2: Not1; Equimolar amounts of mRNA extracted from fundic and pyloric abomasums of 18 and 21 week old steers.
Exposure to Ostertagia ostertagi was initiated at 15 weeks of age. fundic and pyloric abomasum"
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/clone="9BOV45_M02"
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'strain="Holstein"
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                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Environmental Gene Regulation University of Liverpool School of Biological Sciences, The Bioscience Street, Liverpool, United Kingdom, L69 7ZB Tel: +44(0)151-795-4510 Fax: +44(0)151-795-4431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2004)
Contact: Andrew R. Cossins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Williams,D.R., Gracey,A.Y., Martin,S.L., Hughes,M.A., Li,W., Rogers,J. and Cossins,A.R.
Microarray analysis of transcriptional changes during hibernation in the golden mantled ground squirrel, Spermophilus lateralis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S1LH03c19e02f1 squirrel heart library 1 Spermophilus lateralis cDNA clone 19e02 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermophilus lateralis (golden-mantled ground squirrel)
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Seq primer: pflc T7 (5'-AATACGACTCACTATAGGG-3')
                                                                                                                                                                                                                                                                                                                                      Email: cossins@liv.ac.uk
Vector has been trimmed from this EST
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                                                                                                                                                                                                                                                            quality sequence stop: 800.
Location/Qualifiers
/sex="Male & female"
/tissue_type="Heart"
/dev_stage="Adult"
/lab_host="B.coli Electromax DH10B"
/clone_lib="squirrel heart library IT
/note="Vector: pPIC; Site 1: SalI GTCGAG; Site_2: BamHI
GENTCC; Normalized and subtracted cDNA library prepared
from heart of hibernating and summer animals"
                                                                                                                                                                /db_xref="taxon:76772"
/clone="19e02"
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Best Local Similarity:
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                                                                                                                           KEYWORDS
                                                                                                                                            VERSION
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                                                                                                                                                    AGENCOURT 6707465 NIH_MGC_119 5', mRNA sequence.
BM907988
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1109)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                           Homo sapiens (human)
 Unpublished (1999)
                                                                                                                                           BM907988.1 GI:19358367
                                                                                                                                                                                                                                                                 GlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPhe 237
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12767 row: b column: 07
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                            LeuGlyGluAlaIleHisSerGlnThrGluValHisLeuLySThrGlyGlyIleValPro
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                                   ProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAsnLys 160
                                                                                                                                           GCCAGTGGAGTCTCTCAAGTGACCTCTCAGCAATTGCAACTACCATAAAACCAGGACTT
                                                                                                                                                            AlaSerGlyValSerProSerAspLeuSerAlaIleAlaThrThrIleLysProGlyLeu
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                                                                                                                                                                                                                        ProAlaAlaGlnGlnLeuHisArgGluAsnIleGlnArgIleValGlnGluAlaLeuSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=Torgan: brain; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5744934"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        this is a NIH_MGC Library."
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                   Dept. of Molecular Biosciences, School of Veterinary Medicine University of California, Davis 1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA Tel: 530 752 0793 Fax: 530 752 4698 Email: mashultz@ucdavis.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CF114247 765 bp mRNA linear EST 23-JUL-2003
Shultzomica07498 Rat lung airway and parenchyma cDNA libraries
Rattus norvegicus cDNA clone NA4935 5', mRNA sequence.
                                                                                                                                                                                                                    Average Phred score is 20 or better. All poor quality 20) and vector/linker sequence has been removed. High quality sequence stop: 765.
Location/Qualifiers
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Eukaryota; Metazoa;
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CF114247.1 GI:33173962
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           /tissue_type="airway or parenchyma"
/dev_stage="adult"
/dev_stage="adult"
/clone_lib="Rat lung airway and parenchyma cDNA libraries"
/clone_type="cond-rate"
/note="forgan: lung; "Cottor: pGEN-lize(-j; Site_1: Eco RI;
Site_2: Not I; mRNA was isolated from microdissected rat
lung airways and parenchyma tissues."
                                                                                                                                           /strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                              /sex="male"
                                                                                                                       clone="NA4935"
                                                                                                                                                                                       organism="Rattus norvegicus"
                                                                                                                                                                          _type="mRNA"
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 AAGAAGATTAATGTTCAACCTAGAGCACTTTTTCATCATAAACTGGTGCTGGGAATTGAA
Homo sapiens
Homo sapiens
                                                                                          BQ636028
hd03d11.y1 Human Retina
                                BQ636028.1
EST.
                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                  AlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeu
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398 143 338 123 278 103 218 83 158 63 86 43

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Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of human retina for the l
Project: Retbindin, an abundant, novel retinal cDNA and splicing of other retina-preferred gene transcripts
Mol. Vis. 8 (4), 196-204 (2002)
22103461
12107411
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Plate: 03 row: d column: 11
Seq primer: M13RP1_reverse primer (ABI).
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6/331, NIH, Bethesda, I
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Section on Molecular Structure and Function
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                                          LysCysGluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIle
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AAAAAGGAAAAAGAGGAAGGTATTGAGAAGGGGCAAATCCTGTCTTCAGCAGCAGACATT
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301 496 0078
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/note="Organ: Bye; Vector: psport; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ug of total RNA was used for library
construction. A directionally cloned cDNA library in the
psport; vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the SuperScript Plasmid System full
details of which are contained in the manufacturer's
Instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
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Intramural Sequencing
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/dev_stage="Adult"
/lab_host="EMDH10B"
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was performed on the unamplified library at the second of the second context of th
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/mol_type="mRNA"
/db_xref="taxon:9606"
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                 Veterinary Biomedical Sciences University of Edinburgh Email: J.hopkins@ed.ac.uk Plate: 04 row: N column: 08 Seq primer: Ml3reverse High quality sequence stop: 550.
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aries cDNA clone Oa_splbn_04N08
CN823245
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Gossner,A. and Hopkins,J.
Ovine spleen\brain cDNA library
Unpublished (2004)
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EST.
Ovis aries (sheep)
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                    quality sequence start: 6 quality sequence stop: 550. Location/Qualifiers
                                                                                                                                                    /organism="Ovis aries"
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/clone_lib="Sheep spleen\brain_punte="Vector: pSport1"
                             1.08e-106
1045.00
93.51%
88.31%
49.18%
x CN823245
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Cetartiodactyla; Ruminantia; Pecora;
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Matches:
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Indels:
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5', mRNA sequence.
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cora; Bovidae;
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REFERENCE
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                                           l (bases 1 to 661)
Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.I
Matukumalli, L.K.
Construction and Analysis of a cDNA Library Generated Prom
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
Unpublished (2004)
Contact: Richard G. Baumann
Boyvine Functional Genomics Lab
                                                                                                                                                                                                                       Bos taurus
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4057170 BARC
                                                                                                                                                                             Bovinae; Bos.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys
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Cetartiodactyla; Ruminantia; Pecora;
                   Beltsville,
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taurus
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5', mRNA
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cora; Bovidae;
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Location/Qualifiers
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                                                SerAlaIleAlaThrThrIleLysProGlyLeuAlaLeuSerLeuGlyValGlyLeuSer
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                                                                                                              GCTCATGCACTCACTATTAGGTTAACAAATAAGGTAGAATTTCCGTTTTTAGTTCTTTTG
                                                                                                                                AlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuValLeuLeu
                                                                                                                                                                                                                                       TCAGCAGTTGCAACCACCATAAAGCCAGGACTTGCTTTAAGCTTGGGCGTAGGTTTATCG
                                                                                                                                                                                                                                                                                                       AATATTCAACGCATAGTACAAGAAGCTCTCTCTGCCAGTGAAGTCTCTCCAAGTGAACTC
                                                                                                                                                                                                                                                                                                                         AsnIleGlnArgIleValGlnGluAlaLeuSerAlaSerGlyValSerProSerAspLeu
                                                                                                                                                                           TTTAGCTTACAACTGGTAGACCAGTTTAAAAAAGCCCTTCATTCCCCATTCATCACATGGAG
                                                                                                                                                                                             PheSerLeuGlnLeuValGlyGlnLeuLysLysProPheIleProIleHisHisMetGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="8BOV_20020"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="Holstein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
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1038.50
95.48%
91.86%
48.87%
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Matches:
Conservative:
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189 418 169 358 149 298 129 238 109 178 89 118 69 58

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Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt ', -trim_fasta. Vector iden by cross match using options -minmatch 12 -minscore 18 plate: 20 row: 0 column: 20 plate: 20 row: 0 column: 20 plate: 20 row: 0 column: 20 primer: CCTATTTAGGTGACACTATAGAAC
/tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_hoste="BHIOB TonA"
/lab_hoste="BHIOB TonA"
/clone_lib="BARC 8BOV"
/note="Organ: Intestine; Vector: pCMVSport6.1; Site 1:
NotI; Site 2: EcoRI; Normalized cow cDNA intestinal—
library in pCMVsport6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"
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ACCESSION
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KEYWORDS
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Best Local Similarity:
Query Match:
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AUTHORS
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
(LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM13213 row: d column: 19
High quality sequence stop: 674.
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 879)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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BQ433135.1 GI:21172211
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GluPheLeuArgSerPheAsnPheHisProGlyThrLeuPheLeuHisLy8I1eValLeu
                                                                      MetLeuIleLeuThrLysThrAlaGlyValPhePheLysProSerLysArgLysValTyr
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/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH_MGC_92"
/clone_start; Vector: pcMV-SporT6; Site_1: NotI;
/note="Organ: testis; Vector: pcMV-SporT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT_primed.
Average insert size 2.5 kb. Library enriched for
full-length_clones_and_constructed_by_Life_Technologies.
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Search completed: February 16, 2005, 21:04:35 Job time : 4943.95 secs

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GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR00905; Peptidase M22.
AnterPro; IPR00910; Pept M22 Osialgl.
Pfam; PF00814; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialglc pptds; 1.
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Submitted (CCT-2000) to the EMBL/GenBank/DDBJ
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RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Murakami K., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kamehori K., Takahashi-Pujii A., Hara H., Tanase T., Nomura Y.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Noriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Yamazaki M., Watanabe T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Kawabata R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ30879.
Hymon sapiens (Human).
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Best Local S
Matches 361
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MEROPS; M22.004; -..

GO; GO:0008450; F:O-sialoglycoprotein endopeptidase activity; IEA.

GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0008270; F:Zinc ion binding; IEA.

GO; GO:0008270; F:Zinc ion binding; IEA.

InterPro; IPR000905; Peptidase M22.

InterPro; IPR000905; Peptidase M22.

InterPro; IPR009180; Pept M22_Osialgl.

Pfam; PF00014; Peptidase M22; 1.

PIRSF; PIRSF004537; Osialglc_pptds; 1.

PRINTS; PR007389; OSIALOPTASE.

PRODOM; PD002367; Peptidase M22; 1.
SEQUENCE FROM N.A.

STRAIN=CZECH II; TISSITE-Mammary, tumor;

MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler
                                                                                                                                                  Q6PEB4;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                           Hypothetical protein. Mus musculus (Mouse).
                                                                                                Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mizushima-Sugano J., Satoh T., Shirai Y., Okumura K., Kikuchi Nakai K., Yada T., Nakamura Y., Ohara O., "Complete sequencing and characterization
                                                                                                                                                                                                            Q6PEB4
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; AK055441; BAB70923.1; -.
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    Mismatches

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Pred. No. 8.4e-134;
                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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H., Masuho Y., Yamashita R.,
IBogai T., Sugano S.;
of 21,243 full-length human
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EMBL, BCOS8172; AAHSB172.1; -.

GO; GO:0008450; F:O-sialoglycoprotein endopeptidase act
GO; GO:0008270; F:Zinc ion binding; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR009180; Peptidase M22; 1.

R Pfam; PF00814; Peptidase M22; 1.

R PIRSF; PIRSF004537; Osialglc pptds; 1.

R PRINTS; PR00789; OSIALOTASE.
R PRINTS; PR00789; OSIALOTASE.
R PRINTS; PR00789; OSIALOTASE.
R PRINTS; PR00789; OSIALOTASE.
R PIRSF004327; Peptidase M22; 1.
R TIGRENMS; TIGRO329; gcp; 1.
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Best Local S
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Hypothetical protein.
SEQUENCE 414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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IMIAWNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKWBI
                                                                     QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MLMLRRTAGAI PKPPKSKVYGFLRRFSVHPRTLSCHKLVLGIETSCDDTGAAVVDETGNV
                                                                                                                                                                                                                      QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKDGNRFHFTIN
                                                                                                                                                                                                                                                                                            ALSLGVGLSFSLQLVNRFKKPFIPIHHMBAHALTIRLTNKVBFPFLVLLISGGHCLLALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1835; DB 2;
Pred. No. 5.8e-133;
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RESULT Q8BLB6 ID Q

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**987188**0

PRELIMINARY;

PRT;

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C STRAIN-579E/GJ; TISSUE=Corpora quadrigemina;

C Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

A Adachi J., Aizawa K., Akimura T., Arakawa T., Hashizume W.,

A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Nakamura M.,

Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Taqami M.

Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
MEDINE=20530913; PubMed=11076861; D01=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system—384-format
sequencing pipeline with 384 multicapiilary sequencer.";
Genome Res. 10:1757-1771(2000).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
enriched library, clone:B230219017 product:similar to PUTATIVE
SIALOGLYCOPROTEASE TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
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[3]
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Budammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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SEQUENCE FROM N.A.
TISSUE=Corpora
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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Best Local S
Matches 352
Q9DONO;
Q9DONO;
01-JUN-2001
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SEQUENCE
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GO; GO:0008450; F:O-sialoglycoprotein endopeptidase activity; GO:0008233; F:peptidase activity; IEA.

GO; GO:0008270; F:zinc ion binding; IEA.

GO; GO:0006508; F:proteolysis and peptidolysis; IEA.

InterPro; IPR000905; Peptidase M22.

InterPro; IPR009180; Peptidase M22.

InterPro; IPR009180; Peptidase M22; 1.

Pfam; PP00814; Peptidase M22; 1.

PIRSF; PIRSF004537; OsialGl:Dptds; 1.

PRINTS; PR00799; OSIALOPTASE.

PRINTS; PR00799; OSIALOPTASE.

PRINTS; PR00739; OSIALOPTASE.
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                                                                                                                                                                                                                                                         QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK
                                                                                                                                                                                                                                                                                        ALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRLTNKVEFPFLVLLISGGHCLLALV
                                                                                                                                                                                                                                                                                                                                        MLMLRRTAGAI PKPPKSKVYGFLRRFSVHPRTLSCHKLVLGI ETSCDDTGAAVVDETGNV
                                                                                                                                                                                                                                                                                                                                                                                                        MLILTKTAGVFFKPSKRKVYEFLRSFNFHPGTLFLHKIVLGIETSCDDTAAAVVDETGNV
                                                                                                      IMIAWNGIERLRAGIGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI
                                                                                                                                                    THRAILFCKQRDLLFQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNG
                                                                                                                                                                                                     PPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKR
                                                                                                                                        THRAILFCKOKNILSPANAVLVVSGGVASNLYIRKALEIVANATOCTLLCPPPRICTDNG
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                                                                                                                                                                                                                                        QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEQLAKDGNRFHFTIN
                                                                                       IMIAWNGIERLRAGLGVLHDVEDIRYEPKCPLGVDISREVAEAAIKVPRLKMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR00329;
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 (TrEMBLrel.
                         PRELIMINARY;
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29; gcp; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.0%; Score 1827;
85.0%; Pred. No. 2.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 10 days embryo whole body cDNA, RIKEN
                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Whole body;
STRAIN=C9279253; PubMed=10349636; DOI=10.10
Carninci P., Hayashizaki Y.;
"High-efficiency full-length DNA cloning.";
                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                     SIALOGLYCOPROTEASE
                                                                                                                                                                               enriched library,
SEQUENCE FROM N.A.
                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                         Name=Osgepl1;
                        Enzymol.
                        303:19-44 (1999)
                                                                                                                                                                     clone:2610001M19
E TYPE 2.
                                                                                                                      Chordata;
Rodentia;
                                                                                                                                                                                                     17,
17,
26,
                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                product:similar
                                                            DOI=10.1016/S0076-6879(99)03004-9;
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                                                                                                                                                                                full-length
to PUTATIVE
                                                                                                                       Euteleostomi;
; Murinae; Mus
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Query Match
Best Local S
Matches 351
                                                                                                                                    InterPro; IPR000905; Peptidase M22.
InterPro; IPR009180; Pept M22 Osialg1.
Pfam; PF00814; Peptidase M22; 1.
PIRSF; PIRSP004537; Osialg1c_pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
PRODOm; PD002367; Peptidase M22; 1.
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Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.
Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Whole body;

MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new ge
Genome Res. 10:1617-1630(2000).
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                                                                                                                      TIGRFAMs; TIGR00329;
                                                                                                                                                                                                                                                                                                                                 MEROPS; M22.004; -. MGD; MGI:1919335; Osgepl1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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STRAIN=C57BL/6J; TISSUE=Whole
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                    GO:0008450; F:O-sialoglycoprotein endopeptidase activity; IEA. GO:0008233; F:peptidase activity; IEA. GO:0008270; F:zinc ion binding; IEA. GO:0008508; P:proteolysis and peptidolysis; IEA.
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,
RA Stapleton M., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA RAHA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schmerch A., Schein J.B.,
RA Jones S.J., Marra M.A.:
Director MGC Project;

$\text{Submitted (AMT-2004) to the EMBL/GenBank/DUBJ die EMBL; BC078974 AAH78974.1; -.

$\text{CO:} GO:0008450; F:O-sialoglycoprotein endopeptic GO; GO:0008270; F:zinc ion binding; IEA.

$GO; GO:0006508; P:proteolysis and peptidolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein (Fragment).
Rattus norvegicus (Rat).
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25-OCT-2004 (TrEMBLrel.
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Strausberg R.L., Feingold E.A., Grouse L.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                           Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                          mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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28, Last sequence update)
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MEROPS; M22.004; -...Go; GO:0008450; F:O-sialoglycoprotein endopeptidase activity; GO; GO:0008231; F:Deptidase activity; IEA.
GO; GO:0008231; F:zinc ion binding; IEA.
GO; GO:0006270; F:zinc ion binding; IEA.
GO; GO:0006283; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR009180; Peptidase_M22.
Pfam; PF00814; Peptidase_M22; 1.
                                                                                                                                                                                    Babbage A.; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ EMBL; AL591593; CAD43471.1; -.
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Pfam; PF00814; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialglc pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
ProDom; PD002367; Peptidase M22; 1.
TIGRPAMs; TIGR00329; gcp; 1.
PROSITE; PS00435; PEROXIDASE 1; UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
SI:dZ211013.4 (Novel glycoprotease).
Name=dZ72B14.6;
                                                                                                                                                                                                                                                                                                                                                                         Erachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Ostariophysi; Cypriniform
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8JFW3
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InterPro; IPR009180; Pept_M22_Osialg1.
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7955;
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Pred. No. 2e-124;
9; Mismatches 35;
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Best Local Sim:
Matches 242;
                                                                  GO; GO:0008450; F:O-sialoglycoprotein endopeptidase act
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22:
InterPro; IPR009180; Peptidase M22; I.
Pfam; PF00814; Peptidase M22; I.
PIRSF; PIRSF004537; Osialglc_pptds; 1.
PRINTS; PR00799; OSIALOPTASE.
PRODOM; PD002367; Peptidase_M22; 1.
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PRINTS; PR00789; OSIALOPTASE.
ProDom; PD002367; Peptidase_M22; 1.
TIGRFAMs; TIGR00329; gcp; 1.
Protease.
SEQUENCE 404 AA; 43956 MW; 3A6B1
                                                                                                                                                                                                         Submitted (JUN-2003) to the EMBL/GenBank/DDBJ EMBL; AL672217; CAD43443.1; -
MEROPS; M22.004; -
G0; G0:0008450; F:O-sialoglycoprotein endopept G0; G0:0008233; F:peptidase activity; IEA.
G0; G0:0008270; F:zinc ion binding; IEA.
G0; G0:0006508; P:proteolysis and peptidolysis
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sec
01-MAR-2004 (TrEMBLrel. 26, Last am
SI:dZ72B14.6 (Novel glycoprotease).
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Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8JFR7
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                          Protease
                                                    TIGRFAMs;
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                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                 Peptidase_M22;
29; gcp; 1.
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Query Match
Best Local Sin
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Best Local Similarity
Matches 241; Conser
                                                                                                                                 TIGRFAMS;
                                                                                                                                                                      GO; GO:0008450; F:O-sialoglycoprotein endopeptidase GO; GO:0008270; F:zinc ion binding; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22;
InterPro; IPR009180; Pept M22 Osialgl.
Pfam; PF00814; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialgl: pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
PRO0789; PR00789; OSIALOPTASE.
PRO0789; PR00789; Peptidase M22; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (MGS) entry w
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Eukaryota; Metazoa; Arthropoda; Nematocera; Culicoidea; Anopheles.
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Pred. No. 4.2e-51;
8; Mismatches 142
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RA Adams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adamatides P.G., Scherer S.B., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burton G.G., Baxter B.G., Helt G., Nelson C.R., Gabor G.L.,
RA Burtil J.F., Agbayani A., An H.J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bhandari D., Bolshakov S.,
RA Burtis K.C., Bussm D.A., Butler H., Cadieu B., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport J.B., Dietz S.M.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraez G., Ferriera S., Pleischmann W.,
ROJECT C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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01-MAR-2004 (TrEMBLrel. 2
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Bndopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=10731132; DOI=10.1126/science.287.5461.2185;
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Query Match
Best Local Similarity
Matches 156; Conser
                                                                                                                        GO; GC:0008450; F:0-sialoglycoprotein energy; GO; GC:0008270; F:0-sialoglycoprotein energy; GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0006508; P:proteolysis and peptide InterPro; IPR00905; Peptidase M22.
InterPro; IPR009180; Peptidase M22; I.
Pfam; PP00814; Peptidase M22; I.
PIRSF; PIRSF004537; Osialglc pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
PRODOM; PD002367; Peptidase M22; 1.
TIGRFAMS; TIGR00329; GCP; 1.
SEQUENCE 409 AA; 45328 MW; 9797F66E71
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MEDLINE=22426065; PubMed=12537568;

MEDLINE=22426065; PubMed=2 D.A., Kronmiller B., Carlson J.W., Halpern A
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Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22426069; PubMed=12537572; Millburn G.H., Campbell K.S., Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ashburner M., Celniker S.E.;
"The transposable elements of the a genomics perspective.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IntAct; Q9VWD6; -. FlyBase; FBgn0031060; CG14231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2004) to the EMBL; AE003513; AAF49008.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Patel S., Frise E., Wheeler D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Score 714.5; DB 2
Pred. No. 1.3e-46;
0; Mismatches 140
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SEQUENCE FROM N.A., Chan M.M., Chang C.H., Chang E., Dale J.I Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Quach H.L Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Yamam
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core everosids II; Brassicales; Brassicaceae; Arabidopsis.
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d (JAN-2001) to ti
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Ecker J.R.,
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O73H71; Q73H71; PRELIMINARY; rai,
C Q73H71;
T 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
T 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
T 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
B Peptidase, M22 family protein.
B OrderedLocushames=WD0699;
N OrderedLocushames=WD0699;
S Wolbachia pipientls wMel.
C Bacteria; Proteobacteria; Alphaproteobacteria; Rick-
DC Bacteria; Proteobacteria; Wolbachia.
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Best Local S
Matches 154
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GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0008508; F:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR000905; Peptidase M22.
FinterPro; IPR009180; Pept M22_Osialgl.
Pfam; PP00814; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialglc_pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
PRODOM; PD002367; Peptidase_M22; 1.
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Submitted (JUM-2002) to the EMBL/GenBank/DDBJ EMBL; AC002387; AAB82636.2; -.
EMBL; AY024338; AAK00530.1; -.
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PubMed=15024419;
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Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.
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Davis R.W., Ecker
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Ecker J.R.,
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GO; GO:0008270; F:zinc ion binding; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR009180; Pept M22 Osialgl.
Pfam; PP00814; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialgl. pptds; 1.
PRINTS; PR00789; GSIALOFFASE.
PRODOm; PD002367; Peptidase M22; 1.
TIGRFAMS; TIGR00329; gcp; 1.
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Q92LH8;
Q92LH8;
Q1-DEC-2001 (TrEMBLrel. 19, Cro
01-DEC-2001 (TrEMBLrel. 26, Las
01-MAR-2004 (TrEMBLrel. 26, Las
PROBABLE O-SIALOGLYCOPROTEIN EI
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EMBL; AE017258; AAS14395.1; -.
TIGR; WD0699; -.
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Last annotation updat
N ENDOPEPTIDASE (EC 3.
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MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398; Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J. Boistard P., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss B., Lelaure V., Masuy D.,

SEQUENCE PRO

FROM

NCBI\_TaxID=382;

ORFNAmes=SM03230; Rhizobium meliloti (Sinorhizobium meliloti). Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.

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GO; GO:0008450; F:O-sialoglycoprotein endopeptidase activity;
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR00180; Peptidase M22.
InterPro; IPR00180; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialglc_pptds; 1.
STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., F
Watanabe A., Idesawa K., Ishikawa A., Kawashin
Kishida Y., Kiyokawa C., Kohara M., Matsumoto
                                                                                                                                                                                                                                                                                                                                                        01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
0-sialglycoprotein endopeptidase (Gcp).
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ProDom; PD002367; Peptidase_M22; 1.
TIGRFAMs; TIGR00329; gcp; 1.
                                                                                                                                                        SEQUENCE FROM N.A.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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Pred. No. 1.9e-35;
77; Mismatches 133; Indels 47;
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                              Asamizu E., Kato T., Sasar
a A., Kawashima K., Kimura
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GO; GO:0008450; F:O-sialoglycoprotein endopeptidase act
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR009180; Pept M22_Osialgl.
Pfam; PP00814; Peptidase M22; 1.
Pfam; PP00814; Peptidase M22; 1.
PRINTS; PR00789; OSIALOPTASE.
PRINTS; PR00789; OSIALOPTASE.
PRODOM; PD002367; Peptidase M22; 1.
TIGRPAMS; TIGR00329; gcp; 1.
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Best Local :
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 PLD-----SISAPMV 353
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                             GVDISKEVGEASIKVPQL 410
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                                                           IKATLERLCAEAGFIFVAPPLKLCTDNAAMIAWAGIERLREGMA---QENGFDFVPRSRW
                                                                                       IRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPL
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Pred. No. 4
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Search completed: February 16, 2005, 13:08:38 Job time: 79.2 secs

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Minimum DB
Maximum DB
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geneseqD2000s:*
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geneseqD2004s:*
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1923.349 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ហ	4	ω	2	_	No.	Result
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
263	263.5	266.5	268.5	270.5	270.5	270.5	275.5	275.5	276	277	277	277.5	279.5	279.5	279.5	280.5	280.5	289.5	289.5
19.0		19.2	19.4	19.5	19.5	19.5	19.9	19.9	19.9	20.0	20.0	20.0	20.2	20.2	20.2	20.3		20.9	20.9
341	354	338	343	337	325	325	337	337	421	341	309	335	337	337	337	357	340	342	342
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ABU41689	ABU37844	ABM67812	ABO62704	AAY52204	AAY52203	AAR26325	ABU28771	AAU34711	ABG96491	ABU40069	ABU33614	ABU27480	ABU50237	ABU47561	AAU38187	ADF06228	ABU40514	ABU30280	AAU35450
Abu41689	Abu37844	Abm67812	Abo62704	Aay52204	Aay52203	Aar26325	Abu28771	Aau34711	Abg96491	Abu40069	Abu33614	Abu27480	Abu50237	Abu47561	Aau38187	Adf06228	Abu40514	Abu30280	Aau35450
Protein e	Protein e	Photorhab	Klebsiell	Escherich	Pasteure.	Glycoprot	Protein e	E. coli c	Novel hum	Protein	Protein	Protein	Protein	Protein	Salmonel	Bacteria.	Protein	Protein	Haemophil

## ALIGNMENTS

## RESULT 1 ABG96487 Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; munume disorder; rheumatoid arthritis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia; emphysema; cystic fibrosis; vascular disorder; inflammatory disorder; ABG96487 standard; protein; Homo sapiens. Novel human metalloprotease MP1 fragment 11-DEC-2002 ABG96487; neurological disorder. (first entry) 267 À #1.

WO200272751-A2

19-SEP-2002.

05-FEB-2002; 2002WO-US003353.

05-FEB-2001; 10-APR-2001; 2001US-0266518P. 2001US-0282814P.

(BRIM ) BRISTOL-MYERS SQUIBE CO.

Peder J, Nelson TC, Ψ,

Duclos

Krystek

N-PSDB; WPI; 2002-723329/78. DB; ABS76639.

Chen

ç

New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and neurological disorders. neurological

Claim 5; Page 29; 473pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a metalloprotease (MP-1). (I) is useful for preventing, treating, or

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cc aberrant glutamate transport or motor neuron disorder, such as CC amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like condition. The compositions and methods are also useful for diagnosing, CC prognosticating, treating, ameliorating and/or treating disorders CC associated with Mp-1 activity, e.g. diabetes, cancer, reproductive CC disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell CC aplasia), metabolic disorders (e.g. premature puberty, Kallman syndrome, CC or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, Puntington's disease or Tourette syndrome), liver and renal diseases and immune disorders (e.g. AIDS, rheumatoid arthritis CC fibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This is the amino acid CC sequence of a metalloprotease MP1 protein
ARESULT 2
ABG96478
ID ABG9
XX ABG9
XX ABG9
XX Neta
DE Nove
XX Meta
Cus
KW moto
KW repr
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KW park
KW empl
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Albheimer's disease; cushing's syndrome; meurodegenerative disease; Albheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; immune disorder; rheumatoid arthritis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia
    05-FEB-2001; 2001US-0266518P
                                                                                     05-FEB-2002; 2002WO-US003353.
                                                                                                                                                                           19-SEP-2002
                                                                                                                                                                                                                                                        WO200272751-A2
                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                      emphysema; cystic fibrosis; vascular disorder; neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human metalloprotease MP1.
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Pred. No. 1.4e-147;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and
                                                       Human O-sialoglycoproteinase-like protein SEQ ID
                                                                                            19-APR-2002
                                                                                                                               ABB05481;
                                                                                                                                                                     ABB05481 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 414 AA;
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Human; O-sialoglycoproteinase-like

protein; OSGPLP; enzyme

Homo sapiens

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RESULT 4
ABJ26654
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Matches 267
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cerebroprotective; antiparkinsonian; nootropic; antiinflammatory;
antiulcer; hepatotropic; gynaecological; antibacterial; virucide;
protozoacide; antiparasitic; cell proliferative disease; PMOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O-sialogycoproteinase-like for diagnosing, preventing
                                           Cytostatic: antiarteriosclerotic; anti-HIV; antiallergic;
                                                                                                     01-MAY-2003
                                                                                                                                                             ABJ26654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 30-31 (Disclosure); 38pp; Chinese.
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Similarity 100.0%; Pred. No. 2.8e-147;
67; Conservative 0; Mismatches 0;
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                                                                                                                                                             standard;
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                                                                       modification + maintenance molecule protein
                                                                                                                                                            protein; 414
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Local Similarity nes 267; Conserv

100.0%; Score 1385; DB 6; ilarity 100.0%; Pred. No. 2.8e-147; Conservative 0; Mismatches 0;

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Sequence

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The invention relates to an isolated polypeptide comprising: any of 28 CC sequences of 48-1256 amino acids; a natural amino acid sequence at least CC 90% identical to the 28 amino acid sequences, 94% identical to a sequence CC of 703 or 267 amino acids, 96% identical to a sequence of 414 amino CC acids, or 97% identical to a sequence of 242 amino acids, all given in CC the specification; or a biologically active or immunogenic fragment of CC in diagnosing, treating and preventing diseases or conditions associated with the decreased expression of protein modification and maintenance CC molecules (PMOD), such as cell proliferative diseases (e.g. cancer, CC altergoes), neurological disorders (e.g. stroke, Parkinson's disease, CC endometriosis), autoimmune/inflammatory diseases (e.g. AIDS, CC endometriosis), developmental (e.g. ulcer, cirrhosis), reproductive (e.g. centergies), neurological disorders (e.g. stroke, Parkinson's disease, CC endometriosis), developmental (e.g. ulcer, cirrhosis), reproductive (e.g. conceriosis), autoimtestinal (e.g. ulcer, cirrhosis), reproductive (e.g. conceriosis), developmental, vesicle trafficking disorders, and CC infections (e.g. bacterial, viral, parasitic, protozoal). These are also CC useful in assessing the effects of exogenous compounds on the expression of the cragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the craget polymucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. The microarray is useful in monitoring confit in the invention profiles. This sequence represents a human PMOD protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUN-2001; 2001US-0300508P.
06-JUL-2001; 2001US-0303445P.
13-JUL-2001; 2001US-0305405P.
09-AUG-2001; 2001US-0311442P.
24-AUG-2001; 2001US-0314921P.
29-AUG-2001; 2001US-0315992P.
03-MAY-2002; 2002US-0378205P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human PMOD polypeptide and polynucleotide, useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gandhi AR, Kable AE, Swarnakar A, Hafalia AJA, Tran B, Duggai Warren BA, Ison CH, Honchell CD, Nguyen DB, Lu DAM, Lee EA, Forsythe IJ, Barroso I, Ramkumar J, Griffin JA, Li JX, Yang i Thangavelu K, Gietzen KJ, Ding L, Baughn MR, Borowsky ML, Yang Walia NK, Mason PM, Gururajan R, Lee S, Becha SD, Lee SY, Ti Elliott VS, Luo W, Sprague WW, Tang YT, Lu Y, Zebarjadian Y;
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Walia NK, Mason PM,
Elliott VS, Luo W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 63;
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e EA, )
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L, Yao MG;
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                       08-NOV-2001; 2001WO-US051427
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domain"
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/note= "Transmembrane
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                                                                                                                                                                                    note= "Non-transmembrane domain"
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                                                                                                                                                                                                                                                                                                             note= "Transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                            note= "Non-transmembrane domain; non-cytoplasmic loop
                                                                                                                                                                                                                                                                     note= "Non-transmembrane domain; cytoplasmic domain"
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                                                                                                                                            "Sialoglycoprotease type domain"
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                       30-JAN-2003
                                                             ABG71161;
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The present invention relates to novel 38650, 28472, 5495, 65507, 81588 CC or 14354 nucleic acid molecules which encode adenosine deaminase, glyco-cc protease or seven transmembrane domain (77M) receptor family members. CC Sequences of the invention are useful in diagnosing and treating cancer cor lung cancer), immune disorders (e.g. selective IgA deficiency, rheumatoid carthritis, diabetes, allergy), heart or cardiovascular disorders (e.g., thousand in farction, thrombus) including endothelial cell disorders (e.g., psoriassis, Grave's disease), haematopoietic disorders, brain cC disorders (e.g., cerebral oedema, Parkinson's or Alzheimer's disease), classin and metabolic disorders (e.g., obseity), liver disorders or platelet cC (e.g. diagnostic assays, prognostic and therapeutic medicine cC (e.g. diagnostic assays, prognostic and therapeutic methods. The cultivation of the prognostic and therapeutic methods. The conclusion of the injunction are also used in chromosome mapping, tissue typing and collaborate in gene therapy. The present sequence is human glycoprotease.
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Best Local Similarity
Matches 260; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 414 AA;
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08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
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388
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                                                     PKCPLGVDISKEVGEASIKVPQLKMEI 267
                                                                                                             ASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYE
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Pred. No. 4.3e-143;
3; Mismatches 4;
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(first entry)

protein; 414

Cancer; aberrant Novel human

cell proliferation; aberrant cell differentiation;

glycoprotease 28472.

breast cancer; ovarian cancer; prostate cancer; colon cancer; lung cancer; immune disorder; heart disorder; cardiovascular disorder; endothelial disorder; hematopoietic disorder; blood vessel disorder; brain disorder; pain; metabolic disorder; liver disorder; diabetes; platelet disorder; carcinoma; sarcoma; leukaemia; Hodgkin's disease; autoimmune disorder; hypertension, atherosclerosis; heart failure; myocardial infarction; ischaemic heart disease; Crohn's disease; moyocardial infarction; ischaemic heart disease; Crohn's disease; carev's disease; Kawasaki syndrome; Raynaud's disease; anourysm; cerebral ischaemia; peripheral neuropathy; Alzheimer's disease; enzyme.

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CC 14354 nucleic acid molecules (I) and their encoded polypeptides (II). The CC 38650 nucleic acid molecule comprises a sequence encoding adenosine CC deaminase. The 28472 nucleic acid molecule comprises a sequence encoding comprises a sequence encoding a human glycoprotease. The 5495, 65507, 81588 and 14354 comprise CC a human glycoprotease. The 5495, 65507, 81588 and 14354 comprise CC sequences that encode a human seven transmembrane domain (7TM). The CC sequences are useful for diagnosing, preventing or treating a subject CC with or at risk of developing a disorder, e.g. cancer or aberrant CC cellular proliferation and/or differentiation (e.g. breast, ovarian, CC prostate, colon or lung cancer), immune disorders, heart disorders, cardiovascular disorders, endothelial disorders, heart disorders, colond vessel disorders, brain disorders, pain and metabolic disorders, CC liver disorders, brain disorders, pain and metabolic disorders, colond vessel disorders, brain disorders, pain and metabolic disorders, cC liver disorders, brain disorders, autoimmune disorders, cC sarcoma, leukaemia, Hodgkin's disease, autoimmune disorders, Kawasaki CC syndrome, Raynaud's disease, Crohn's disease, Kawasaki CC syndrome, Raynaud's disease, aneurysm, cerebral ischaemia, peripheral cachexia or diabetes. This is the amino acid sequence of the novel human collocation of the collection of the movel human collocation.
   Query Match
Best Local S
Matches 260
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08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
                                                                                                                                             Sequence
                                                                                                                                                                                                                     glycoprotease
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                                           Local Similarity
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leic acids and polypeptides, designated 38650, 28472, 5495, 65507,
88 and 14354, useful for treating e.g. leukemias, Hodgkin's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention describes isolated 38650, 28472, 5495, 65507, 81588 and
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138. .152
/label= Glycoproteas
                                       97.3%;
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•-
Score 1348; DB
Pred. No. 4.3e-1
3; Mismatches
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                            8; DB 6;
4.3e-143;
                                                                    Length 414;
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MEAHALTIRLTNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR

0

Gaps

The invention relates to an isolated 38650 (encoding adenosine deaminase), 28472 (encoding a glycoprotease), 5495 (encoding a 7 transmembrane receptor), 65507, 81588 or 14354 nucleic acid molecule (or a sequence which is at least 60% identical to the six nucleic acids or their open reading frames, fragments of at least is nucleotides, naturally occurring variants, or a DNA insert of the plasmid deposited with the American Type Culture Collection as Accession No. not defined in the specification, which encodes the amino acid sequence). Also included are a host cell containing the nucleic acids (used to produce the

60

Conservative

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RRSULT 7
ABU09 11D ABU09
XX ABU00
XX ABU00
XX ABU00
XX Huma
XX Huma
XX Huma
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XX Iive
XX Ion
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XX US20
XX Homo
XX ION
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                                                                                                                                                                                                                                                                                                                                            New isolated 38650, 28472, 5495, 65507, 81588 and 14354 nucleic acid molecules, useful for diagnosing, treating cancer, pain, or immune, heart, endothelial cell, hematopoeitic, blood vessel, brain, metabol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-NOV-2000; 2000US-0246768P.
08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; enzyme; cancer; aberrant cellular proliferation; differentiation; immune disorders; heart disorder; brain disorder; cardiovascular disorder; endothelial cell disorder; pain disorder; haematopoeitic disorder; blood vessel disorder; metabolic disorder; liver disorder; platelet disorder; glycoprotease.
                                                                                                                                                                                                                                                                  Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leiby KR,
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(KAPE/) KAPELLER-LIBERMANN
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                                                                                                                                                                                                                                                                                                                      liver disorders.
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                                                                                                                                                                                                                                                                  Fig 8; 90pp;
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RESULT 8
ADA54471
ID ADA55
XX ADA5
AC ADA5
XX ADA5
XX Cyto
XX Cyto
XX Gene
XX Gene
XX Homo
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XX 11-8
PD 19-M
XX 21-M
XX 21-M
XX 14-8
PR 24-J
XX 14-8
PR 24-J
XX 18-9
PR 14-8
PR 24-J
XX 18-9
PR 18-9
XX WPI;
DR N-PS;
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DR N-PS;
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Best Local
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                                                        Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                 Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease.
              WPI; 2003-395539/38.
N-PSDB; ADA52832.
                                                                                                                                                                  14-SEP-2001;
24-JAN-2002;
                                                                                                                                                                                                              21-MAR-2002; 2002EP-00006586
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Similarity 97.4%;
60; Conservative
                                                                                                                    HELIX RES INST.
RES ASSOC BIOTECHNOLOGY.
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                                                                                                                                                                  2001JP-00328381.
2002US-0350435P.
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                                                        Otsuki T,
Hio Y, Ots
Otsuka M,
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Pred. No. 4.3e-143;
3; Mismatches 4;
                                                        T, Wakamatsu A, Sa
Otsuka K, Nagai K,
M, Nagahari K, Masu
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K, Irie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for disease which the gene is involved, or as target molecules for gene therapy.
                                                Disclosure; SEQ ID NO 34191; 21pp + Sequence Listing; English
                                                                                                                            New isolated nucleic a
genes from Drosophila
                                                                                                                                                                                                           WPI; 2001-656860/75.
N-PSDB; ABL13236.
                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                             (PEKE ) PB CORP NY
                                                                                                       interactions.
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2000US-00614150.
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98.6%;
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Pred. No. 1.1e-115;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                       Myers
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an isolated nucleic

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Best Local Similarity 38.2
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY52216 standard; protein; 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57377-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                         Region
                                                                                                                                                                                                                      Region
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                                                                                                                                                                                                                                                                                                                                                              ygjD protein; essential; Gram positive; Gram negative; identification; antagonist; antibacterial; antibiotic; treatment; infection; resistance; drug target.
                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana ygjD protein homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY52216;
                                                22-APR-1998;
                                                                             20-APR-1999;
                                                                                                              28-OCT-1999
                                                                                                                                             WO9954470-A2
                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
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                 (GLAX ) GLAXO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFC--KQRDLLPQNNAVLV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASTRYDYD---SIDIOGSAGFA 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRIRLHILPEYRLWNGGRAIEHAAQLASDPLAYEFPLPLAQQRNCNFSFAGIKNNSFRAI
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                 GROUP
                                                9868-00008423.
                                                                               99WO-EP002635.
                                                                                                                                                                                          /note= "ygjD conserved
208. .259 
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                                                                                                                                                                                                                                                                   "ygjD
                                                                                                                                                                        "ygjD conserved motif 1"
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Pred. No. 1.4e-37;
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broad spectrum;
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Best Local S
Matches 100
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 25-FEB-1999;
05-MAR-1999;
                                                                                                                                                          Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                        AAG19287;
                                                                                                                                                                                                                                                                                                                                                                        AAG19287 standard; protein; 245 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteins AAY52202-Y52217 encompass a novel family of proteins designated the ygjD family, after the mame given to the Escherichia coli family member. These proteins are essential for the survival of both Gram negative and Gram positive bacteria, although no function has as yet been ascribed to these proteins. The ygjD proteins, fragments of ygjD proteins
                                                   25-FEB-2000;
                                                                                         06-SEP-2000
                                                                                                                          EP1033405-A2
                                                                                                                                                                                             termination sequence
                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment
                                                                                                                                                                                                                                                                                                     17-OCT-2000
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                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
 Arabidopsis thaliana
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nilarity 38.7%;
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nilarity 38.7%;
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; 9908-01	20-JUL-199	PR	, 99US-01.	21-APK-1999;	
, 9908-01	19-001-195	- F	TO-SOR6 ;	19-APK-1999;	
TO-SOR6 :	361-70P-61	- F	, 9908-01.	10 APR-1999;	
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, 9908-01	12-JUL-199	PR			
9908-01	09-JUL-195	PR	; 2000EP-00301439.	25-FEB-2000;	
; 99US-01	08-JUL-195	PR			
; 99US-01	06-JUL-199	PR		06-SEP-2000.	_
; 99US-01	02-JUL-199	PR			
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99115-01	23-JIN-190	g g			
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23-SEP-1999;
24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
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                                                                                                        AVLVASGGVASNFYIRRALBILTNATQCTLLCPPPRLCTDNGIMIAWNGIBRLRAGLGIL 231
                                                                                                                                                                                                                                                                                                RLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK
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99US-0161992P.
99US-0161993P.
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0159329P.
0159330P.
0159331P.
0159637P.
0159634P.
0159634P.
0160741P.
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-0153758P.
-0154018P.
-0154039P.
-0154779P.
-0155139P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 444;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Ehrlichia ruminantium polynucleotides, useful as vaccines for inducing protective immunity, and protecting animals or humans against rickettsial diseases, e.g. typhus, spotted fever or heart water.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 251 AA;
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Moreland AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-2002
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LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKK 120
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                                                                                      KYIDN----
                                                                                                                                        EKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAI-----LFCKQRDLLPQNNAVLV
                                                                                                                                                                                                 LNL-GYP-----ĠĠPIİEKKSIMĞDSKSFFLPRALINRLGCDFSFSĞIKTAVRNİVVNQ
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L, Mwangi
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                                                                                      ---DFICNISASFQDCIGDILVNRITNAIHMSQAINCKINK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.7%; Score 342; DB 5; 34.8%; Pred. No. 1.4e-29;
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Mcguire TC,
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Mahan SM;
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The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense CC nucleic acid; (2) a host cell containing the vector; (3) an isolated CC polypeptide or its fragment whose expression is inhibited by the containing the vector; (3) an isolated CC polypeptide; (5) producing the polypeptide; (6) inhibiting cellular CC proliferation or the activity of a gene in an operon required for CC the gene product or that has an activity against a biological pathway CC required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological CC pathway in which a proliferation-required gene or its gene product lies CC or a gene on which the test compound that inhibits gene product lies CC or a gene on which the test compound that inhibits proliferation of an CC compound's activity; (11) a culture comprising strains in which the gene CC product is overexpressed or underexpressed; (12) determining the extent CC which each of the strains is present in a culture or collection of Strains; or (13) identifying the target of a compound that inhibits the gene CC product of the strains. The antisense nucleic acids are useful for identifying proteins or accepting how accepting the cardidate molecules for rational CC drug discovery programs, or for screening bandledges mucleic acids required corrections of accepting to isolate candidate molecules for rational CC drug discovery programs.
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Wall
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID NO 50858; 1766pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isolate
discovery programs, or for screening homologous nucleic acids ired for proliferation in cells other than S. aureus, S. typhin
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Forsyth RA,

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                                                                                                                                                                                                                                                                                                                                                                  Sequence 382 AA;
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                                                                                                                                                                                                                                                                                                             Similarity
GVGANALLRAHLARALKPLRAEAYFPPLSLCTDNGAMIAFAAAERVKAGLADLRE 363
                             GVASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHD
                                                                                                                                                LMGL-GYP----
                                                                       KAATRDGGELGE--QDRADLAAATQAAIVEVLAAKAIRAL---KQTGL-----RRLVVAG
                                                                                                          KKEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASG 178
                                                                                                                                                                                                                                                                                                           23.2%; Score 321.5; DB 6
37.4%; Pred. No. 5.6e-27;
                                                                                                                                              -GGPALARLAEQGDASRYDLPRPMLHSGDLDFSFSGLKTAVLTRV--
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Search completed: February Job time: 55.6902 secs 13:05:56

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Result
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

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US-09-543-681A-6513
US-09-543-681A-6513
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US-10-087-997-2
US-09-189-039A-9221
US-09-189-132A-6609
US-08-987-121A-4
US-10-084-52
US-09-188-110-4857
US-10-066-512-2
US-09-533-110-4857
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Sequence 19, Appli
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Sequence 2726, Ap
Sequence 17372, Ap
Sequence 17372, Ap
Sequence 6513, Ap
Sequence 4, Appli
Sequence 28, Appli
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Sequence 4857, Ap
Sequence 4956, Ap
Sequence 1956, App
Sequence 1956, Ap
Sequence 1956, App
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US-S-S-S-S-S-S-S-S-S-S-S-S-S-S-S-S-S-S-		
RESULT 1  Sequence 22,  Sequence 22,  Patent No. 6  GENERAL INFO,  APPLICANT:  TITLE OF IN  TITLE OF IN  TITLE OF IN  FILE REFERE  CURRENT APPL  CURRENT APPL  PRIOR APPLI  PRIOR FILIN  ORGANISM:  ORGANISM:  US-10-067-443-		22200000000000000000000000000000000000
RESULT 1 US-10-067-443-22 ; Sequence 22, Appli ; Patent No. 6642041 ; Patent No. 6642041 ; Patent No. 6642041 ; Patent No. 6642041 ; Patent No. 6642041 ; Patent No. 10 INVENTIO ; PILE REFERENCE: D ; CURRENT APPLICATION ; PRIOR APPLICATION ; PRIOR APPLICATION ; PRIOR PILING DATE ; PRIOR FILING DATE ; PRIOR APPLICATION ; PRIOR FILING DATE ; PRIOR APPLICATION ; PRIOR		194 169 169 169 194.5 94.5 94.5 94.5 94.5 94.5 94.5 94.5
SULT 1  Sequence 22, Application US/10067443 Sequence 22, Application US/10067443 Sequence 22, Application US/10067443 Sequence 22, Application US/10067443 Sequence 22, Application US/10067443 GENERAL INFORMATION: SQUIDE CONTINE OF INVENTION: POLYNUCLEOTIDE TITLE OF INVENTION: SPINAL CORD, M FILE REFERENCE: D0073 MP CURRENT APPLICATION NUMBER: US/10/0 CURRENT FILING DATE: 2002-02-05 PRIOR APPLICATION NUMBER: US 60/266 PRIOR FILING DATE: 2001-02-05 PRIOR APPLICATION NUMBER: US 60/282 PRIOR FILING DATE: 2001-04-10 NUMBER OF SEQ ID NOS: 71 SOFTWARE: PatentIn version 3.0 SEQ ID NO 22 LENGTH: 267 TYPE: PRT ORGANISM: homo sapiens		114.0 113.1 112.2 5.0 6.8 5.7 5.7 5.7 5.7
lication Usinion State of Consider of Cons		.340 .143 .292 .214 .480 .481 .108 .326 .336 .336 .345 .345 .356 .356 .356 .356 .356 .356 .356 .35
S/10 Squi Squi Squi UCLE AL C 2-02 US 2-03 US 4-10		/ a,aaaaaaaaaaa
pany ENCODING 19-1 67,443 ,518	ALIGNMENTS	US-10-067-443-6 US-09-328-352-4609 US-09-724-623-81 US-09-724-623-81 US-09-583-110-5050 US-09-107-433-3197 US-09-902-540-15572 US-09-902-540-15572 US-09-910-779-3008 US-09-110-779-3008 US-09-110-779-3108 US-09-110-779-3118 US-09-110-79-3118 US-09-110-79-918-31118 US-09-252-9918-31118 US-09-252-9918-22790 US-08-609-0498-13 US-09-170-996-13
NOVEL ME		1387 1609 1050 1050 1057 1057 1057 1057 1057 1057
A NOVEL METALOPROTEASE HIGHLY EXPRESSED		Sequence 6, 3 Sequence 438: Sequence 460: Sequence 505: Sequence 319: Sequence 5. 38: Sequence 5. 40: Sequence 5. 40: Sequence 5. 40: Sequence 7, 3 Sequence 313: Sequence 313: Sequence 227: Sequence 313: Sequence 227: Sequence 227:
11СНГУ ЕХ		6, Appli 4387, Ap 4387, Ap 4609, Appl 5050, Ap 5050, Ap 13197, Ap 15572, A 5, Appli 15572, A 5, Appli 7, Appli
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Query Match
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Matches 267
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PKCPLGVDISKEVGEASIKVPQLKMBI 267
                                                                     ASNFYIRRALBILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYE
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RESULT 2 US-10-067-443-2

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                                                                                US-10-067-443-19
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CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                      Sequence 19, Application US/10067443
Patent No. 6642041
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
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                                                                                              LENGTH: 439
TYPE: PRT
ORGANISM: homo
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CURRENT FILING DATE: 2002-02-05
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                               Score 1358.5; DB 4
Pred. No. 1.4e-156;
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                  Mismatches
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; TYPE: PRT ; ORGANISM: Arabidopsis thaliana US-10-067-443-3
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
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DPPPPATEPEDYVYDLRPRWPLGEEYAKGRSEA
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                                                                                                                                                         VASNEYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRY 239
                                                                                                                                                                                                                                                              KEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGG 179
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                                                  PKCPLGVDISKEVGEA
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; ORGANISM: M.catarrhalis
US-09-540-236-2726
                                                                                                                                                                                                                                         ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17372
                                                                                                                                                           Query Match
Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
FILE REFERENCE: 107196.752 991A
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CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2726
LENGTH: 350
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SEQ ID NO 17372
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APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 6 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                     LENGTH:
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87; Conserve
                                     60 PLSLIKUPECSTWSGGKAIEHLAKQGWKFHFDIKFFLHHAKNCDFSFTGLQHVTDKIIMK 119
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                                                                              MEGHLLAPMLEEQPPRFPFVALLVSGGHTQLVRVDGIGRYQLLGESVDDAAGEAFDKTAK 231
                                                                                                                 MEAHALTIRLTNK-VBFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAFGDMLDKVAR 59
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                                                                                                                                                         21.0%; Score 291.5; ilarity 35.4%; Pred. No. 1.6c Conservative 37; Mismatches
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-GGPEIARLAERGTPGRFVFPRPMTDRPGLDFSFSGLKTFTLN-TWO 283
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US-08-087-797-3
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LENGTH: 357
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FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Proteus mirabilis
                                                                               APPLICANT: Mellors, Alan
APPLICANT: Lo, Reggie Y.C.
APPLICANT: Lo, Reggie Y.C.
TITLE OF INVENTION: Pasteurella Haemolytica
TITLE OF INVENTION: Glycoprotease
TITLE OF INVENTION: Gene and the Furified Enzyme
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson, P.A.
STREET: 1211 East Morehead Street,
                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                         Application US/08087797
                                                                                                                                                                                                                                                                                                                                                                                         TVRPRWPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVSANRTLRAKMAMIMEQLGGEVFYARPELCTDNGAMIALAGMIRFKGGTEGPL----GV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NDDSB-----QTRADIARAFEDAVVDTLAIKCRRA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.3%; Score 280.5; DE 32.7%; Pred. No. 3e-25;
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US-10-067-443-4
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            APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REPERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                             Sequence 4, Application US/10067443
Patent No. 6642041
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEDITIN Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,797
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
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Local Similarity 33.6%;
hes 83; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Layton, Jr., Samuel G. REGISTRATION NUMBER: 22807
REFERENCE/DOCKET NUMBER: 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLGL-DYP-----GGPLLSKMAAQGTAGREVFPRPMTDRPGLDFSFSGLKTFAANTIRD 224
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; TYPE: PRT
; ORGANISM: Caenoxhabditis elegans
US-10-067-443-28
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-04-10 NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0
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Sequence 28, Application US/10067443
Patent No. 6642041
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED IN
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
                                                                                                                                                                                                                                                                    117 IMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 MRAHALSILLVDDSVRFPFSAVLLSGGHALISVAEDVEKFKLYGQSVSGSPGECIDKVAR
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                                                                                                                                                                                                   RIRKNSETSID-----IPDFCASLQNTVARHISSKIHIFFESLSEQEKLPKQ---LVI 302
                                                                                                                                                                                                                                                                                                                                     QLGDL-GSEFDGIHVGAAVEILASRASADGHLRYPIFLPNVPKANMNFDQIKGSYLNLLE
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                                                                 GGGVAANQYIFGAISKLSAAHNVTTIKVLLSLCTDNAEMIAYSGL-
                                                                                                                                  SGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.9%; Score 276; DB 4; Length 421; ilarity 30.4%; Pred. No. 1.4e-24; Conservative 52; Mismatches 107; Indels
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-KCPLGVDISKEVGEASIKVPQLKM 265
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                                                                       LMLVNRSEA 356
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                                                              US-09-489-039A-9221
                                                                                 RESULT 12
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                     Sequence 9221, Application US/09489039A Patent No. 6610836
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: '704 334 2014
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: LAYTON, Jr., Samuel G.
REGISTRATION NUMBER: 22807
REFERENCE/DOCKET NUMBER: 337-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,797
FILING DATE: 14-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mellors, Alan
APPLICANT: Lo, Reggie Y.C.
APPLICANT: Abdullah, Khalid M.
TITLE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS: ADDRESSEE: Bell, Seltzer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Abdullantifie OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 70% 334 2014
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                                                                                                                                                                                      180
                                                                                                                                           274 VSANKQLRADLAEMMKKLKGEVFYPRPQFCTDNGAMIAYTGFLRLK 319
                                                                                                                                                                                                                                                                                                                                                                                               112 MEGHLLAPMLEENAPEFPFVALLISGGHTQLVKVDGVGQYELLGESIDDAAGEAFDKTGK 171
                                                                                                                                                                                                                                                                                                                                                    60 RLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK 119
                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEAHALTIRL-TNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVAR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79;
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: No. 5543312th Carolina
                                                                                                                                                                                   VASNFYIRRALBILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLR 225
                                                                                                                                                                                                                            NLNENGELDEQ---TKCDIAHAFQQAV-----VDTILIKCK-RALEQTGYKRLVMAGG
                                                                                                                                                                                                                                                                     KEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGG 179
                                                                                                                                                                                                                                                                                                              LLGL-DYP-----AGVAMSKLAESGTPNRFKFPRPMTDRPGLDFSFSGLKTFAANTIKA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  704 377 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.5%; Score 270.5; DB 1; Length 325; 35.0%; Pred. No. 4.2e-24; ative 26; Mismatches 102; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene
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Glycoprotease
Gene and the Purified Enzyme
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d Street,
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RESULT 13
US-09-107-532A-6609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6609, Application US/09107532A
Patent No. 6583275
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9221
LENGTH: 343
TYPE: PRT
ORGANISM: Klobsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
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                                                              APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1337
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                     APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGDDE-----QTRADIARAFEDAVVDTLMIKCRRA-----LEQTGFKRLVMAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK 119
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                      NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                      SOPTWARE: ASCII
                                                                                                                                                                                                                                                                                                            COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSES: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.4%; Score 268.5; DB 4; 32.7%; Pred. No. 8.1e-24; tive 31; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7310
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TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-50 TELEFAX: (781)893-8277

(781)893-5007

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US-08-987-121A-4
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GENERAL INFORMATION:
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                    TELEPHONE: 317-276-3334
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 6609: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                          REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hoskins, Jo Ann
APPLICANT: Tang, Joseph Chiou-Chung
APPLICANT: Treadway, Patti Jean
TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence
SEQUENCE
                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                NAME: Webster, Thomas D. REGISTRATION NUMBER: 39,872
                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Lilly Corp. CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...363
SEQUENCE DESCRIPTION: SEQ ID NO: 6609:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 MAGHIYAARLVKPFQFPLMALLVSGGHTELVYMQEDGSYBIIGETRDDAAGEAYDKVGRV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LSLIKHPECSTMSGGKAIEHLAKQG-NRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGL-----SYPSGKEIDQLAHQGKDNYHF--PRAMIHEDNYDFSFSGLKSAFINLVHN 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08987121A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGVAANQGLREGLQAALSAKLPEVELVIPPLRLCGDNAAMI 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 363 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                   Indiana
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                                                                                                                                                                                                                   US/08/987,121A
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                                                                                                                                                                                                                                                            Version
                                                                                                                                                                                                                                                              #1.30
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-987-121A-4
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Query Match 18.:
Best Local Similarity 32.0
Matches 72; Conservative
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Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local :
                                                                                                                                                                                     TELEFAX: (301) 309-851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: HP Vectra 486/
OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Choi et.
TITLE OF INVENTION:
                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                            STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Rockville
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                                                                                                                                                                   LENGTH:
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6159469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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HP Vectra 486/
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                                                                                                                                                                                                                                            (301)
                                                                                           protein
                   18.1%; Score 250; DB 3; 32.0%; Pred. No. 1.4e-21;
                                                                                                                                                                                                                                            309-8504
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                                    Length 335;
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36;

Mismatches

Indels

30;

Gaps

8

Search	В	δλ	DЬ	Ş	망	Ş	рb	92
Search completed: February 16, 2005, 13:10:25	272 AANKGLRERLAAEITDVKVIIPPLRLCGDNAGMIAYASVSXWN 314	181 ASNEYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWN 219	226 EQKGESLST-EDLCASFQAAVMDILMAKTKKALEKYPVKILVVAGGV 271	121 EKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGV 180	174 MGLTYPAGREIDELAHQGQDI-YDFPRAMIKEDNLEFSFSGLKSAFINLHHNA 225	61 LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKK 120	114 MAGHLMAAQSVEPLEFPLLALLVSGGHTELVYVSEAGDYKIVGETRDDAVGEAYDKVGRV 173	1 MEAHALTIRLTNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR 60

Search completed: February 16, 2005, 13:10:2 Job time : 16.962 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                 1358.5
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1385
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10T_NEW_PUB.pep:*
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6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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US-10-067-443-22
US-10-649-273-22
US-10-651-722-22
US-10-649-273-2
US-10-649-273-2
US-10-667-443-19
US-10-667-43-19
US-10-667-43-19
US-10-651-722-19
US-10-651-722-19
US-10-697-443-2039
US-10-994-749-2039
US-10-0424-599-209259
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                                                                                                                           Sequence 2, Appli
Sequence 2, Appli
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Sequence 19, Appli
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Sequence 22, App.
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10-282-122A-5	-10-282-122A-696	-10-282-122A-65	-122A-566	-815-242-103	-10-651-722	-10-651-	-10-649-	-10-649-273-	0	-10-067-443-	-10-282-122A-679	-10-282	10-282-122A-5540	-10-282-122A-7816	-282-122A-	US-09-815-242-13780	6843	-282-122A-58	09-815-242-11	-282-122A-66	0	-10-01	-10-282-122A-6	0-282-122A-6315	-10-282-122A-	-10-012-140-2	-10-282-122A	ŗ	US-10-437-963-113732	US-10-651-722-3	US-10-649-273-3
57817,	e 69613	e 65768,	æ	.03	Sequence 28, Appl	4	28	4	28, App	4	e 67993,	61538,	55404,	78161	e 75485,	13780,	68438,	e 58204,	H	e 662	1179	24, App	672	63156	e 44499,	e 25, App	e 50858,	е9,	e 1	e 3, Appl	Sequence 3, Appli

## ALIGNMENTS

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Publication No. US20030082782A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 22
LENGTH: 267
TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                            Query Match 100.0%; Score 1385; DB 14; Length 267; Best Local Similarity 100.0%; Pred. No. 1.8e-139; Matches 267; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED IN
TITLE OF INVENTION: SPINAL CORD, MP-1
PILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/262,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.0
  121 EKBEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLFQNNAVLVASGGV 180
                                                        61
                                                                           51 LELIKHPECSTWGGGKÄIEHLÄKGGNRFRIFDIKFFLÄHÄKNCUPSFTGLGHVTDKIIMKK 120
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CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
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Sequence 22, Application US/10651722
Publication No. US20040048302A1
GENERAL, INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PILING DATE: 2001-02-05
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LENGTH: 267
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE,
FILE REFERENCE: D0073 CNT
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SOFTWARE: PatentIn version 3.2
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100.0%; Pred. No. 1.8e-139;
vative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/067,443;
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOPTWARE: Patentin version 3.0
SETURE 141
TYPE: PRT
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Matches
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Publication No. US20030082782A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
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PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
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                                                                                                                                                                                                                               Query Match
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                                         LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKK
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Sequence 2, Application US/10651722

Publication No. US20040048302A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A 1
FILE REFERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
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CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
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Publication No. US20040043407A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE,

FILE REFERENCE: D0073 CNT
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PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-067-443-19
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Publication No. US20030082782A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    SOPTWARE: PatentIn version 3.0 SEQ ID NO 19
                                                                                                                                                                                       Matches 266; Conservative
                                                                                                                                                                                                      Query Match 98.1%;
Best Local Similarity 91.1%;
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/667,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER: OF SEQ ID NOS: 71
NUMBER: OF SEQ ID NOS: 71
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Best Local :
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                                                                                                                                                                                                                                                                             LENGTH: 439
TYPE: PRT
ORGANISM: homo sapiens
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                                                                                                            1 MEAHALTIRLTNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR 60
                                                                        LSLIKHDECSTMSGGKAIEHLAKQUKEREDIKEPLHHAKNCUESFIGLQHVTDKIIMKK 120
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   EKBEGI ---
                                        LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPFLHHAKNCDFSFTGLQHVTDKIIMKK
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                                                                                                                                                                                   Score 1358.5; DB 14
Pred. No. 2.5e-136;
0; Mismatches 1;
 --EKGQILSSAADIAATVQHTMACHLVKRTH 155
                                                                                                                                                                                                                         DB 14; Length 439;
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US-10-651-722-19
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Sequence 19, Application US/10651722

Publication No. US20040048302A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1

FILE REFERENCE: D0073 DIV

CURRENT APPLICATION NUMBER: US/10/651,722

CURRENT FILING DATE: 2003-08-29

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR FILING DATE: 2001-02-05
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PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
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Best Local Similarity 91.1%;
Matches 266; Conservative
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CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: homo sapiens
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PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
LENGTH: 439
TYPE: PRT
ORGANISM: homo sapiens
US-10-651-722-19
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US-10-012-140-5
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CURRENT FILING DATE: 2001-11-08
PRIOR PELICATION NUMBER: 60/246,768
PRIOR PELING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR FILING DATE: 2000-11-08
PRIOR PELICATION NUMBER: 60/249,185
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                       Query Match
Best Local
                                                                                                                                                                                                              SEQ ID NO 5
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Best Local !
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TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, A
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 381552004900
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                                                                                                                                                          TYPE: PRT
ORGANISM: Homo
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Local Similarity 91.1%;
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                                                                                     Similarity
MEAHALTIRLTNKVBFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR
                  MEAHALTIRLTNKVBFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR 60
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                                                                      Conservative
                                                                                                                                                              sapiens
                                                                                     97.3%;
97.4%;
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                                                                   Score 1348; DB 14;
Pred. No. 3.1e-135;
3; Mismatches 4;
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 207
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APPLICANT: NAGAHARI, KENJI
APPLICANT: MAGSHAO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER: OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2039
LENGTH: 364
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2039
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US-10-094-749-2039
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Local Similarity 98.6%;
   181
                                                                                                                                                                       148 MEAHALTIRLTNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR 207
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                                                                                                                      61 LSLIKHPECSTMSGGKAIEHLAKQGNREHFDIKPPLHHAKNCDPSFTGLQHVTDKIIMKK 120
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 ASNFYIRRALBILTNATQCTLLCPPPRLCTDNGIMIA 217
                                 EKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLFQNNAVLVASGGV 180
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
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YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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ISONO, YUUKO
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    Mismatches

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Pred. No. 2.6e-109;
0; Mismatches 3;
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                                                  SEQ ID NO 3
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US-10-067-443-3
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Publication No. US20030082782A1
GENERAL INFORMATION:
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APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REPERENCE: 38-21(53223)B
CURRENT TAPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 209259
                                                                                                                                                                                                                                                                           APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: STRAL CORD, MP-1
FILE REFERENCE: D0073 NP
FILE REFERENCE: D0073 NP
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ORGANISM: Arabidopsis thaliana
                                                LENGTH: 463
TYPB: PRT
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ORGANISM: Glycine max
FEATURE:
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Local Similarity 41.6%; Pred. No. 4.1e-36;
hes 104; Conservative 32; Mismatches 89; Indels 25;
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CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10649273
Publication No. US20040043407A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLBOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
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Best Local Similarity
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TYPE: PRT
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                                                              VASNKYVRLRLNNI VENKNLKLVCPPPSLCTDNGVMVAWTGLEHFRVG---
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                                                                                                                                                KE-----IRNRADIAASFQRVAVLHLBEKCERAIDWALE---LEPSIKHMVISGG
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36.6%; Pred. No. 1.1e-34;
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PKCPLGVDISKBVGEA 256
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Publication No. US20040048302A1
GENERAL INFORMATION:
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PRIOR TILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
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404 DPPPPATEPEDYVYDLRPRWPLGEEYAKGRSEA 436
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                                               -PKCPLGVDISKEVGEA 256
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Search completed: February 16, 2005, 13:28:30 Job time: 155.686 secs

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Result
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-MODEL-frame+ p2n.model -DEV=Xlh
-MODEL-frame+ p2n.model -DEV=Xlh
-MODEL-frame+ p2n.model -DEV=Xlh
-Q-/Ggn2_1/USPTO_Spool/US10649273/runat 14022005_114702_16399/app_query.fasta_1.1429
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXX=0
-UNITS-bits -START=1 -EXD=-1 -MARTX=blosum62 -TRANS=human40.cdi -LIST=45
-DCGALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=200000000
-USER-US10649273_@CGN 1 1 8655_@runat_14022005_114702_16399 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MĀIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPD=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Fgapop 6.0 , Fgapext
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## ALIGNMENTS

Alignment Scores: pred. Mo.: Score: Percent Similarity: Best Local Similarity: Query Match:	TITLE I JOURNAL I FEATURES SOURCE ORIGIN	SOURCE ORGANISM URGENERENCE AUTHORS	z Q
y: rity:	Wang, D. and Wucleic acid Vucleic ic acid Patent: Usc 1. /mo	Unknown. Unknown. Unclassified. I (bases 1 to 1416) Tang,Y.T., Zhou,P., Zhang,J., Zhao,Q.A.,	AR541929 Sequence 177 from paten AR541929 AR541929.1 GI:53934009
1.37e-126 1385.00 100.00% 100.00%	Wang, D. and Drmanac, R.T.  Nucleic acids and polypeptides  Patent: US 6743619-A 177 01-JUN-2004;  Location/Qualifiers  11416  /organism="unknown" /mol_type="genomic DNA"	to 1416) hou,P., Goodri	i i
Length: Matches: Conservative: Mismatches: Indels:	ides 1-JUN-2004; rs n" c DNA"	Unknown. Unknown. Unknown. Unclassified. Unclassified. I (bases I to 1416) Tang,Y.T., Zhou,P., Goodrich,R., Liu,C., Asundi,V., Ren,F., Zhaug,J., Zhao,Q.A., Yang,Y., Xue,A.J., Wehrman,T., Wang,JR.,	1416 bp DNA US 6743619.
1416 267 0		Asundi,V., Wehrman,T.,	linear
		Ren, F., wang, JR.,	PAT 08-OCT-2004

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RESULT 2
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Sequence 23
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AR428809.1
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Unclassified.

1 (bases 1 to 1526)

1 (bases 1 to 1526)

Chen, J., Feder, J.N., Nelson, T.C., Krystek, S.R. and Duclos, F. Polynucleotides encoding a novel metalloprotease, MP-1
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                                                                                                                                                ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal
                                                                                                                                                                      ATTGAAAGACTACGTGCTGGCTTGGGCATTTTACATGACATAGAAGGCATCCGCTATGAA
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                                      ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal
                                                                     LeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGly
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Location/Qualifiers
1. .1526
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Strausberg, R.L., Feingold, E.A., Grouse, I.H., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gumaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gequencing Center (NISC),
Gaithersburg, Maryland;
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov
Akhter, N. Ayele, K., BeckstromSternberg, S.M., Benjamin, B.,
Blakesley, R.W., BeckstromSternberg, S.M., Benjamin, B.,
Blakesley, R.W., BeckstromSternberg, S.M., Benjamin, B.,
Blakesley, R.W., BeckstromSternberg, S.M., Haghighi, P.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
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Hansen, N., Ho, S.-L., Karlins, B., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Massiello, C., Masker, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Volume, A., Wetherby, K.D., Wiggins, L.,
                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 28 Row: i Column: 22.
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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On Dec 19, 2003 this sequence version replaced
                                                                                                                                                                                                                                                                                                                          Young, A., Zhang, L.-H. and Green, B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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VEFPFLVLLISGGHCLLALVQGVSDFSLLGKSLDIAPGDMLDKVARRLSLIKHPEGST
MSGGKALBHLAKQGNRFHFDIXFPLHHAKUCDFSFTGLQHVTDKIIMKKEKEBGIEKG
QILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIR
RALBILTNATQCTLLCPPPRLCTDNGIMIAMNGIERLRAGLGILHDIEGIRYEPKCPL
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/db_xref="CDD:pfam00814"
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/lab_host="DH10B-R"
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/mol_type="genomic |
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Chen, J., Feder, J.N., Nelson, T.C., Krystck, S.R. and Duclos, F.
Polynucleotides encoding a novel metalloprotease, MP-1
Patent: US 6642041-A 21 04-NOV-2003;
Location/Qualifiers
1. .1387
                                                                                                                                                                                                                                                                                                                                Unknown
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                                                                         Cloning and sequencing of a second human sialoglycoprotease homologue unpublished
                                                                                                                                                                              HSA295148
HGmo sapiens mRNA for putative sialog AJ295148
AJ295148.1 GI:11071726
metallopeptidase; sialoglycoprotease.
                   Direct Submission
Sübmitted (27-GCT-2000) Chen J.M., MRC Molecular Bnzymology
Laboratory, The Babraham Institute, Babraham, Cambridge, CB2 4AT,
                                                      2 (bases 1 to 1387)
Chen, J.M.
                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                               Homo
          UNITED
                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                               AlaSerIleLysValProGlnLeuLysMetGluIle 267
                                                                                                                                                                                                                                                                                                                                          GlyIleArgTyrGluProLysCysProLeuGlyValAspIleSerLysGluValGlyGlu 255
                                                                                                                                                                                                                                                                                                                                                                                        | IleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGlu
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                                                                                                                                                            sapiens
          KINGDOM
Location/Qualifiers
                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                    sialoglycoprotease
                                                                                                  human putative
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                                                                                                                                                                                                                                                                                                                 GluLysGluGluGlYIle-----
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TENT BGCITTUHTGTSVENGEN
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REFERENCE
AUTHORS
TITLE
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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LeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys 100
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Sequence 4
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                                                                                                                                                                                                       Millennium Pharmaceuticals, Inc.
Location/Qualifiers
                                                                                                                                                                                                                             of human proteins and uses thereof Patent: WO 02074960-A 4 26-SEP-2002;
                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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                                                                                                                                              /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
146...1390
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            GVDISKEVGEASIKVPQLKMBI"
                                                                                                   /codon_start=1
/protein_id="CAD80044.1"
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Leiby, K.R., Kapeller-Libermann, R. and Glucksmann, M. 38650, 28472, 5495, 65507, 81588 and 14354 methods
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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NGGGKAIEHLAKQGNRFHFDIKPELLLGKSLDIAPGDMLDKVARRLSLIKHPECST
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RALEILTNATQCTLLCPPPERLCTDNGIMIAMNGIERLRAGLGILHDIEGIRYEPKCPL
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SOURCE
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Willalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Boutfard, G.G., Blakesley, R. W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Paragas, P. (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 123 Row: d Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312463.
                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.(
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web sire. here: (NISC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (15-SEP-2003) National Institutes of Health, Mammalian Submitted (15-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
NIH-MGC Project URL: http://mgc.nci.nih.
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
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Mammalia; Eutheria; Rodentia;
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                   /tiosuc_type-"Mammary immor metastatized to immg. The arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." (clone_lib="NCI_CGAP_Lu29"
                                                                                                                    /clone="MGC:67870 IMAGE:5012054"
                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                            db_xref="taxon:10090"
                                                                                                                                                                 strain="CZECH II"
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Sciurognathi; Muridae;
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ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe 160
                                                                                                                                                                                                                                                                                                                           GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla 140
                                                                                                                                                                                                                                                                                                                                                                                                          AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg
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                                                                                        AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr 200
                                                                                                                                                                             CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal
                                                                                                                                              TGCAAGCAGAAAAATTTGCTATCTCCAGCTAACGCAGTATTAGTTGTATCTGGAGGTGTT
                                                                                                                                                                                                                          .GCGGTACAGCATGCAACAGCGTGCCACCTTGCAAAAAGAACACATCGTGCTATTCTGTTT 1142
                                                                                                                                                                                                                                                                                                         GAAAAAGAAGAAGGCATTGAGAAAGGGGCAAATCCTGTCATCAGCTGCAGACATTGCTGCT 1082
                                                                                                                                                                                                                                                                                                                                                                                     AATTGCGATTTTTCTTTTACGGGACTTCAACATATTACTGATAAGCTAATAACACACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="QRI7; Region: Metal-dependent proteases
possible chaperone activity [Posttranslational
modification, protein turnover, chaperones]"
/db_xref="CDD:COG0533"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSGGKAI EHLAKDGNRFHFTINPPMQNAKNCDFSFTGLQHITDKLITHKEKEEGIEKG
QILSSAADIAAAVQHATACHLAKRTHKAILFCKQKNLLSPANAVLVVSGGVASNLYIR
KALEIVANATQCTLLCPPPRLCTDNGIMIAMNGIERLRAGLGVLHDVEDIRYEPKCPL
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RITPSDLSAIATTIKPGLALSLGVGLSFSLQLVNRFKKPPIPIHHMBAHALTIRLTNK
VEFPPLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECST
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Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hisiao, Marcin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smaillus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-OCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                 Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                           Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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                             AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr 200
                                                                                                                                                              CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal 180
                                                                                                                                                                                                                     ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe
                                                                                                                                                                                                                                                                             GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla 140
                                                                                                                                                                                                                                                                                                                                      AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys 120
                                                                                                                                                                                                                                                                                                                                                                              TIGGCCAAAGACGGAAATAGATTCCATTTTACTATCCACCTATGCAGAATGCTAAG
                                                                                                                                                                                                                                                                                                                                                                                               LeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lone distribution: MGC clone distribution information can be fo hrough the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.goveries: IRAK Plate: 86 Row: f Column: 12.
 IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu
                                                                                                                                                                                                       GCGGTACAGCATGCAACAGCGTGCCACCTTGCGAAAAGAACACATCGCGCTATTCTGTTT
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                                                                                                                                                TGCAAGCAGAAAATTTGCTCTCCCAGCTAACGCAGTATTAGTTGTATCTGGAGGTGTT
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/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B"
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clone="IMAGE:5053559"
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Sequence 400 from Patent
AX713716
AX713716.1 GI:29888642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent: EP 1293569-A 400 19-MAR-2003;
Helix Research Institute (JP) ; Resea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                     LeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys 100
  GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla 140
                            ASDCYSASPENSETENCTHISTYFEGGINHISVALTHIASPLYSIEFIEMECLYSLYS 120
                                                                                                                                                         LeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHis
                                                                                                                                                                                                                       LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg
                                                                                                                                                                                                                                                                              LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu 40
                                                                                                                                                                                                                                                                                                                        ATGGAGGCTCATGCACTTACTATTAGGTTGACCAATAAAGTAGAATTTCCTTTTTTAGTT
                                                                                                                                                                                                                                                                                                                                       MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal
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                                                                                                                                                                                                        CTTCTTGGAAAGTCTTTGGACATAGCACCAGGTGACATGCTTGACAAGGTGGCAAGAAGA
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Shihari, K., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Marakami, K., Yasuda, T., Iwayanagi, T., Wagateuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Shiratori, K., Tarahashi, M., Kanda, K., Yokoi, T., Puruya, T., Kikawa, B., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tarihashi, T., Yamashita, H., Minata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Pujii, A., Takauchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Moniyana, H., Satoh, N., Takamabe, T., Sugiyama, A., Satoh, N., Takamabe, T., Sugiyama, A., Satoh, N., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Phuzumi, Y., Pujimori, Y., Komatakami, T., Yamada, K., Fujii, Y., Ozaki, K., Tirani, Y., Kohani, R., Kawakami, T., Kobatake, N., Itahura, S., Moniyama, H., Sasaki, M., Watanabe, T., Nakajawa, K., Sanba, T., Matsunaha, K., Tujii, Y., Satoh, T., Shigeta, K., Sanba, T., Matsunaha, K., Pujii, Y., Satoh, T., Shigeta, K., Sanba, T., Matsunaha, K., Pujii, Y., Komatsu, T., Mizushina-Sugano, J., Satoh, T., Shigeta, K., Sanba, T., Matsunaha, K., Nagase, T., Nomura, N., Kikuchi, H., Masaha, K., Okamura, K., Nagase, T., Nakamashi, Y., Nakagawa, K., Okamura, K., Nakagawa, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5441
Sapiens cDNA FLJ30879 fis, clone FEBRA2004592, highly similar sapiens mRNA for putative sialoglycoprotease type 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishikawa, T., Otsuki, T., Sugiyama, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) MEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 (bases 1 to 2208)
Isogai,T., Otsuki,T. and Sugiyama,T.
Direct Submission
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LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg
                                                                                                              LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu
                                                                                                                                                                                                                     MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal
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/protein_id="BAB70923.1"
/protein_id="BAB70923.1"
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VEFFLVLLISGGHCLHALVQGVSDFFLLLGKSLDIAPGDMLDKVARRLPLIKHPECSTT
MSGGKAIEHLAKQGNRFHFDIKPFLHHAKNCDFPFTGLQHVTDKIIMKKEKEEGIEKG
QILSSAADIAATVQHTMACHLVKRTHRALIFCKQRDLLPQNNAVLVASGGVASNFCIR
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="unnamed protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="brain"
/clone_lib="FEBRA2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="cloning vector: pME18SFL3"
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RS Strausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.R., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Villalou, D.K., Wuzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1436
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Rattus norvegicus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
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IMAGE:7111906,
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AUTHORS
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                                                                                          US-10-649-273-2_COPY_148_414 (1-267)
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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LIMI at: http://image.llnl.gov Series: IRAK Plate: 182 Row: f Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Express Genomics CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 942 Meb site: http://www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (02-AUG-2004) National Institutes of Health, Mammalian Submitted (02-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Proc. Natl. Acad. Sci. U.S.A. 9
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INSMLRVLTALTEDLDSVSSTHTVAHSPLNSGSRGANIQTSMCSCTQTVYMRTVRHTL
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/clone_lib="NIH_MGC_237"
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TITLE
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USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, University of CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
NNA Sequencing by: Institute for Systems Biology
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Mus musculus, clone IMAGE:1327545,
BC051211
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 1109)
                                                                                                                                      Submitted (14-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                Strausberg, R.
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                                                                                                                           31 Center Drive,
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                           ValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCys
                                                                                                                                             AlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeu 159
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              GTTGCAAGTAACTTGTACATCCGAAAAGCATTGGAAATTGTCGCAAATGCAACGCAGTGC
                                                                     TTTTGCAAGCAGAAAATTTGCTCTCTCCAGCTAACGCAGTATTAGTTGTATCTGGAGGT
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/clone_lib="Soares_thymus_2NbMT"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:1327545"
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAR Plate: 113 Row: b Column: 1 This clone was selected for full length sequencing because it This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Brin Helton, Mark Ketteman, Anura
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                         PheLeuValLeuLleSer----GlyGlyHisCysLeu--
TTTTTGATGTTACGTATTGCGTGTATTGGCTTGCATATTTTGAACCATCCCTATATCTCT
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Gallus gallus
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Gallus ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection, from a library constructed by Blizabeth Bosch. cDNA was prepared from RNA extracted from muscle, normalised, and poly A-trimmed. EcoRI-NotI cut cDNA was then ligated into the vector. Vector: poliumscript II KS(+); Site_1: EcoRI; Site_2: NotI Host: Eschericle collinging the control of the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging the collinging th
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BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boardman, P.E., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S.E., Croning, M.D.R., Davies, R.M., Francis, M.D., Grafham, D.V., Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren, S.R., Niblett, D., Overton, I.M., Rogers, J., Scott, C.E., Taylor, R.G., Tickle, C. and Wilson, S.A.

Direct Submission
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/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="ChEST189i14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Gallus gallus"
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                                                        CCAAAAGCTCCCCTTGGAATTGATATTTCCAAAAGAGTTGAAGAGGATTCCATCAAAGTG
                                                                            ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal
                                                                                                                           TTTCTGTCTCCTCCAAGGCTGTGCACCGATAATGGTGTTATGATTGCATGGAATGGC
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Search completed: February 16, 2005, 18:02:51 Job time: 4263.78 secs

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-MODEL-frame+_p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US1649273/runat_14022005_114702_16389/app_query.fasta_1.1429
-Q=/cgn2_1/USPTO_spool/US1649273/runat_14022005_114702_16389/app_query.fasta_1.1429
-DB=N_Geneseq_16Dec04_OFMT=fastap_-SUFFIX=ring_-MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits_START=1 -END=-1 -MATRIX=blosum62_TRANS=human40.cdi
-LIST=45_-DOCALIGN=200_-THR_SCORE=pct_-THR_MAX=100_-THR_MIN=0_-ALIGN=15
-MODE=LOCAL_GUTFMT=pco_-NORM=ext_-HEAPSIZE=500_-MINLEN=0_-MAXLEN=200000000
-USER_US10649273_GCGN_1_1_1057_Grunat_14022005_114702_16389_-NCPU=6_-ICPU=3
-NO_MMAP_-LARGEQUERY_-NEG_SCORES=0_-WAIT_-DSPBLOCK=100_-LONGLOG_-DEV_TIMEOUT=120_-WARN_TIMEOUT=30_-THREADS=1_-XGAPOP=10_-XGAPEXT=0.5_-FGAPOP=6_-FGAPEXT=7_-YGAPOP=10_-YGAPEXT=0.5_-DELOP=6_-DELEXT=7_
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Aca51431 Prokaryot	ACA51431	œ	1014	•	79.	45
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Ų١	ADF02056	10	1074	٠	80.	43
Aca44384 Prokaryot	ACA44384	œ	1020	•	280.5	42
4	ADT05644	13	85814	•	82.	41
Adt05493 Haemophil	ADT05493		9967	20.4	82.	40
1069 Human pro	ABV61069	υı	372	20.6	285	39
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	ACA34150		1029	•	89.	37
Aas53309 Haemophil	AAS53309	4.	1029		9	36
	ADG73343	10	1026	•	89.	36
	ABD02197	1	1206	•	91.	34
3d 0	ABD02280	11	1059	•	91.	33
41	ADG73341	10	1026	•	91.	32
2146 Prc	ACA42146	œ	1026	21.0		31
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0383 M. c	ABQ90383	6	1092	•	30	29
	ABK37804	σ	1000	•		28
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ω P	ACA43173	œ	1032	•	304.5	26
103120 DNA enc	ADL03120	N	1053	•	307	25
_	AAF28551		94750	22.3	308.5	24
N	ACA39102		1044	•	308.5	23
	ACA20445	œ	936	•	314.5	22
4	ACA26804		1146	•	321.5	21
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9	AAD48239	ტ	4360	•	342	19
54 Arabidop	AAC38454	w	1557	٠	Ē	18
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26 DNA up-r	ADL86726	12	371	•	468	15
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5508 Murine	ABQ75508	σ	1572		983	12
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4627 Human	ADQ24627	12	2890	•	1204	10
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## ALIGNMENTS

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PN W021
PF 29-1 Human; gene; ss; nervous system disorder; peripheral neuropathy; Huntington's disease; amyotrophic lateral sclerosis; haemophilia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; autoimmune disease; Parkinson's disease; rheumatoid arthritis; ainsulin-dependent diabetes mellitus; anaenia; thrombocytopaenia; wound; insulin-dependent diabetes mellitus; anaenia; thrombocytopaenia; wound; ulcer; burn; bone disorder; osteoporosis; osteoarthritis; stroke; fibrosis; reperfusion injury; infection; allergic rhinitis; asthma; coagulation disorder; cancer; tumour; inflammatory disease; septic shock; coagulation disorder; cancer; tumour; inflammatory disease; septic shock; ABX70950 standard; cDNA; 1416 BP. WO200281731-A2 Homo sapiens. haemostatic; Crohn's disease; anaphylaxis; proliferation; chemotactic; differentiation; stem cell growth factor; haematopoiesis; chemokinetic; Novel human cDNA sequence #175. 05-MAR-2003 ABX70950; (first entry) antiinflammatory; expressed sequence

Result No.

Score

Query Match

Length DB

1385 1385 1385 1385 1385

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ABX70950 ADS76639 ABA93268 ABS76635 ABT23207

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29-JAN-2002; 2002WO-US001222.

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CC Alzheimer's disease); autoimmune disease (e.g. systemic lupus

CC erythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus)

CC erythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus)

CC enders, burns; bone disorders (e.g. anaemia and thrombocytopaemia)

CC osteoarthritis); mechanical and traumatic disorders (e.g. stroke, head

CC trauma); lung or liver fibrosis; reperfusion injury in various tissues;

CC bacterial, viral or fungal infections; allergic conditions such as

CC allergic rhinitis, asthma; coagulation disorders (e.g. haemophilia);

CC cancer and tumours; and inflammatory diseases (e.g. septic shock, Crohn's

CC disease, anaphylaxis). The protein may be used to inhibit the growth,

CC viruses, or to effect bodily characteristics, biorhythms or circadian

CC cycles of rhythms. The protein may also have

CC proliferation, differentiation, stem cell growth factor, haematopoiesis

CC regulation, immune stimulating or suppressing, chemotactic/chemokinetic,

CC haemostatic and thrombolytic, receptor/ligand, and antinflammatory

CC activities. The cDNA sequences of the invention are useful for expressing

CC recombinant protein for analysis. The present sequence represents a novel

CC human cDNA sequence of the invention, this sequence is an expressed

CC sequence tag (EST) and was identified using subtractive hybridisation
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to the cDNA sequences encoding an isolated novel human polypeptide. The protein encoded by the nucleic acid of the invention is useful for treating central and peripheral nervous system diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic lateral sclerosis); neurodegenerative diseases (e.g. parkinson's disease, hatchard sclerosis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptide useful for treating neurodegenerative diseases, my or lymphoid cell disorders, bone disorders, mechanical and traumatic disorders, coagulation disorders, and inflammatory diseases.
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Xue AJ, Yang Y,
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LeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys
                                                       LeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHis
                                                                                                                  LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg
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                                                                                                                                                   CTTTTGATTTCTGGAGGTCACTGTCTGTTGGCATTAGTTCAAGGAGTTTCAGATTTTCTG
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 Chen J,
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                                                                                                                                                                                                                             Homo
05-FEB-2001; 2001US-0266518P.
10-APR-2001; 2001US-0282814P.
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                                                                          05-FEB-2002; 2002WO-US003353
                                                                                                                           19-SEP-2002.
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BRISTOL-MYERS SQUIBB CO

Feder J,

Nelson TC,

Duclos

'T)

Krystek

2002-723329/78.

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cc metalloprotease (MP-1). (I) is useful for preventing, treating, or can ameliorating a medical condition, particularly an immune disorder, an cc aberrant glutamate transport or motor neuron disorder, such as cc amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like condition. The compositions and methods are also useful for diagnosing, c prognosticating, treating, ameliorating and/or treating disorders (e.g. kleinfelter's syndrome, genital warts, or germinal cell clasorders (e.g. kleinfelter's syndrome, genital warts, or germinal cell caplasia), metabolic disorders (e.g. premature puberty, Kallman syndrome, or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, Cc parkinson's disease, Huntington's disease or Tourette syndrome), liver c and renal disease and immune disorders (e.g. pneumonia, emphysema or cystic cor sepsis), pulmonary diseases (e.g. pneumonia, emphysema or cystic cor sepsis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This sequence represents a metalloprotease MP1 polynucleotide
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes an isolated nucleic acid molecule (I) encoding metalloprotease (MP-1). (I) is useful for preventing, treating, or
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                                                                                                                    O-sialogycoproteinase-like protein and encoding polynucleotide, useful for diagnosing, preventing and treating related diseases.
                                                                                                                                                                                                                                                                                                                                                      Human;
                                                                                                   Claim 5; Page 29-30 (Disclosure); 38pp; Chinese.
                                                                                                                                                                                                               19-APR-2000; 2000CN-00106834.
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/product= "O-sialoglycoproteinase-like
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protein in screening its agonist, excitomotor and inhibitor and preparing an antibody against the CCCPLF protein; and (5) the use of the USGPLP polymcleotide sequences, proteins, agonists, excitomotors, inhibitors and antibodies in treating diseases related to the abnormal OSGPLP gene and in preparing the medicine composite for the treatment

The present sequence encodes human O-sialoglycoproteinase-like protein (OSGPLP). The present invention also describes: (1) the preparation of the OSGPLP protein; (2) applying the OSGPLP protein in diagnosis; (3) the prevention and/or treatment of related diseases; (4) utilising the OSGPLP

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Best Local Similarity:
ABS76635
                      ABS76635 standard;
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Conservative:
Mismatches:
Indels:
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Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; fimmune disorder; rheumatoid arthritis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia; emphysema; cystic fibrosis; vascular disorder; inflammatory disorder;
                                                                                                                                                                                                                                                                                                                                                                                    05-FEB-2002; 2002WO-US003353
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Chen 05-FEB-2001; 2001US-0266518P. 10-APR-2001; 2001US-0282814P. (BRIM ) Ġ BRISTOL-MYERS SQUIBB Feder J, Nelson TC, S Duclos Ţ Krystek S

metalloproteinase activity, neurological disorders. New isolated nucleic acid encoding MP-1 protein, useful for preventing treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and P-PSDB; ABG96478.

2002-723329/78.

Claim 1; Fig 1A-C; 473pp; English.

metalloprotease (MP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder, an aberrant glutamate transport or motor neuron disorder, such as amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like condition. The compositions and methods are also useful for diagnosing, prognosticating, treating, ameliorating and/or treating disorders associated with MP-1 activity, e.g. diabetes, cancer, reproductive disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell aplasia), metabolic disorders (e.g. premature puberty, Kallman syndrome, or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, Parkinson's disease, Huntington's disease or Tourette syndrome), liver and renal diseases and immune disorders (e.g. AIDS, rheumatoid arthritis The invention describes an isolated nucleic acid molecule (I) encoding metalloprotease (MP-1). (I) is useful for preventing, treating, or or sepsis), pulmonary diseases (e.g. pneumonia, emphysema or cystic fibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This sequence represents metalloprotease MP1 polynucleotide

Sequence 2197 BP; 681 A; 441 Ç 439 G 636 Ħ, 0 G. 0 Other;

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Alignment :
Pred. No.:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                               Score:
                                               Scores:
8.75e-147
1385.00
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                               Matches:
         Mismatches:
Indels:
                        Conservative:
2197
267
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US-10-649-273-2\_COPY\_148\_414 (1-267) × ABS76635 (1-2197)

MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal 20

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RESULT 5
ABT723707
ID ABT72
XX
XX
AC ABT72
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DT 01-M
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gastrointestinal; developmental; vesicle trafficking disorder; infection; protein-protein interaction; drug-target interaction; gene expression profile; human; gene; ds.
                                                                                         cérebroprotective; antiparkinsonian; nootropic; antiinflammatory; antiulcer; hepatotropic; gynaecological; antibacterial; virucide; protozoacide; antiparasitic; cell proliferative disease; pMOD; protein modification and maintenance molecule; immunogenic fragment; cancer; autoimmune; inflammatory disease; neurological disorder; cancer; autoimmune; inflammatory disease; neurological disorder;
                                                                                                                                                                                                                                                                            Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; anticonvulsant;
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Percent Similarity: Best Local Similarity: Query Match:

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Conservative: Mismatches: Indels:

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The invention relates to an isolated polypeptide comprising: any of 28 cc sequences of 48-1256 amino acids; a natural amino acid sequence at least composition of 28 telentical to the 28 amino acids sequence, 94% identical to a sequence of 173 or 267 amino acids, 96% identical to a sequence of 414 amino composition of 28 acids, or 97% identical to a sequence of 414 amino composition of 267 amino acids, 96% identical to a sequence of 414 amino composition of 27% identical to a sequence of 414 amino composition of 27% identical to a sequence of 414 amino composition of 28% identical to a sequence of 414 amino composition of 28% identical to a sequence of 414 amino composition of 28% identical and polymoclectides are useful composition of 28% identical and polymoclectides are useful composition of protein modification and maintenance compositions associated compositions of protein modification and maintenance compositions (e.g. bacterial flammatory diseases (e.g. cancer, compositions), neurological disorders (e.g. stroke, Parkinson's disease, compositions (e.g. bacterial, viral, parasitic, proteozoal). These are also compositions (e.g. bacterial, viral, parasitic, proteozoal). These are also composited in assessing the effects of exogenous compounds on the expression composition of nucleic acid and amino acid sequences of pMOD. The pMOD or its composition of the polypeptides, or in altering the expression of the carget polymucleotide and compounds that specifically bind to or modulate the activity of the polypeptides. The microarray is useful in monitoring compositions, and compositions, and compositions, and composition of the invention of the inv
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06-JUL-2001; 2001US-0303445P.
13-JUL-2001; 2001US-0305405P.
09-AUG-2001; 2001US-0311442P.
24-AUG-2001; 2001US-0318921P.
29-AUG-2001; 2001US-0315992P.
03-MAY-2002; 2002US-0378205P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated human PMOD polypeptide and polynucleotide, useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis
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Human; adenosine deaminase; seven transmembrane domain receptor; cancer; 7TM; glycoprotease; immune disorder; 19A deficiency; allergy; arrhythmia; rheumatoid arthritis; diabetes; atherosclerosis; cardiovascular disorder; hypertension; ischaemic heart disease; obesity; myocardial infarction; emdothelial cell disorder; Grave's disease; psoriasis; brain disorder; Parkinson's disease; haematopoietic disorder; cerebral oedema; metabolic disorder; liver disorder; platelet disorder;
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ATGGAGGCTCATGCACTTACTATTAGGTTGACCAATAAAGTAGAATTTCCTTTTTTAGTT MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal

646

LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu

Percent Similarity: Best Local Similarity:

1348.00 98.50% 97.38% 97.33%

Conservative: Mismatches: Indels: Length: Matches:

Gaps:

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The present invention relates to novel 38650, 28472, 5495, 65507, 81588
CC or 14354 nucleic acid molecules which encode adenosine deaminase, glyco-
CC protease or seven transmembrane domain (77M) receptor family members.
CC Sequences of the invention are useful in diagnosing and treating cancer
CC or aberrant cellular proliferation and/or differentiation (e.g. colon or
CC lung cancer), immune disorders (e.g. selective IgA deficiency, rheumatoid
CC arthritis, diabetes, allergy), heart or cardiovascular disorders (e.g.,
CC hypertension, atherosclerosis, arrhythmias, ischaemic heart disease,
CC myocardial infarction, thrombus) including endothelial cell disorders
CC (e.g. psoriasis, Grave's disease), haematopoietic disorders, brain
CC disorders (e.g. cerebral oedema, Parkinson's or Alzheimer's disease),
CC pain and metabolic disorders (e.g. obesity), liver disorders or platelet
CC disorders. They are also useful in screening assays, predictive medicine
CC (e.g. diagnostic assays, prognostic assays, monitoring clinical trials
CC and pharmacogenetics) and prophylactic and therapeutic methods. The
CC consoic biology and as surrogate markers. Sequences of the invention are
                                                                                                                                                                                                                                                                                                                                                                                                                                    New 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules, useful for diagnosing and treating cancer, immune, cardiovascular, hematopoietic, brain, pain, metabolic, liver or platelet disorders, a
                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 8; 178pp; English
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08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
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6 in claim 1 of the specification"
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                                                                                                                                                                             Human; ss; gene; cancer; aberrant cellular proliferation; differentiation; immune disorders; heart disorder; brain disorder; cardiovascular disorder; endothelial cell disorder; pain disorder; haematopoeitic disorder; blood vessel disorder; metabolic disorder; liver disorder; platelet disorder; glycoprotease.
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                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated 38650 (encoding adenosine CC deaminase), 28472 (encoding a glycoprotease), 5495 (encoding a 7 CC transmembrane receptor), 65507, 81588 or 14354 nucleic acid molecule (or cx sequence which is at least 60% identical to the six nucleic acids or CC a sequence which is at least 60% identical to the six nucleic acids or CC their open reading frames, fragments of at least 15 nucleotides, CC maturally occurring variants, or a DNA insert of the plasmid deposited CC with the American Type Culture Collection as Accession No. not defined in CC the specification, which encodes the amino acid sequence). Also included are a host cell containing the nucleic acids (used to produce the protection), the encoded proteins, an antibody that selectively binds to the polypeptide, and identifying a compound that binds to/modulates the activity of the polypeptide. The nucleic acid molecules, polypeptides and CC methods are useful for diagnosing, treating cancer, aberrant cellular CC proliferation and/or differentiation, immune disorders, heart disorders, cardiovascular disorders including endothelial cell disorders, pain CC cardiovascular disorders, blood vessel disorders, brain disorders, pain CC and metabolic disorders, blood vessel disorders, brain disorders (many cx sequence is the Human cDNA 28472 encoding a glycoprotease
                                                                                                                                                                                                                                                                                                                Score:
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08-NOV-2000;
15-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated 38650, 28472, 5495, 65507, 81588 and 14354 nucleic acid molecules, useful for diagnosing, treating cancer, pain, or immune, heart, endothelial cell, hematopoeitic, blood vessel, brain, metabolic and liver disorders.
                                                                                                                                                                                                                                                                                                                                                                            Sequence 1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Fig 8; 90pp; English
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(KAPE/) KAPELLER-LIBERMANN
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                                                                                                                                                            Cancer; aberrant cell proliferation; aberrant cell differentiation; breast cancer; ovarian cancer; prostate cancer; colon cancer; lung cancer; immune disorder; heart disorder; cardiovascular disorder; endothelial disorder; heart disorder; blood vessel disorder; brain disorder; pain; metabolic disorder; liver disorder; diabetes; platelet disorder; carcinoma, sarcoma; leukaemia; Hodgkin's disease; autoimmune disorder; hypertension; atherosclerosis; heart failure; myocardial infarction; ischaemic heart disease; Crohn's disease; Grave's disease; Kawasaki syndrome; Raynaud's disease; aneurysm; cerebral ischaemia; peripheral neuropathy; Alzheimer's disease; cone:
                                                                                                                     Homo
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                                                                  Location/Qualifiers 147. .1391
               /*tag= a
/product= "Glycoprotease 28472"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New adenosine deaminase, glycoprotease and seven transmembrane domain nucleic acids and polypeptides, designated 38650, 28472, 5495, 65507, 81588 and 14354, useful for treating e.g. leukemias, Hodgkin's disease
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08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
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LeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHis
                                        LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg
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                 Iscgai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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24-JAN-2002; 2002US-0350435P.
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Hio Y, Otsuka K, Nagai K, Irie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples and comparing the expression in the first soft tissue samples the level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                    Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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                                                                                        diagnostic and therapeutic polynucleotide; dithp; antiarteriosclerotic; antiinflammatory; cerebroprotective; antiinflammatory; cerebroprotective; antiinpaemic; antidiabetic; immunosuppressive; neuroprotective; nootropic; neuroleptic; tranquilizer; osteopathic; antiarthritic; antirheumatic; cytostatic; hepatotropic; virucide; haemostatic; anti-HIV; antithyroid; thyromimetic;
gene therapy; protein
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thrombolytic; anticoagulant; anorectic; vasotropic; antiulcer;
                                                                                                                                                                                                                                                                             Human diagnostic and therapeutic polynucleotide (dithp), SEQ ID No 100.
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                                                                                                                                                                                                                                                                                                                                      (first entry)
replacement therapy;
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Homo sapiens.

WO2003062376-A2.

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comprising a naturally occurring polynucleotide sequence at least 90% identical to the dithp polynucleotide, a polynucleotide shich is at least 90% identical; or an RNA equivalent of any of the polynucleotides mentary cantivative, an RNA equivalent of any of the polynucleotides mentary cantivative; an RNA equivalent of any of the polynucleotides mention above. The dithp polynucleotides have the following activities: antidiabetic, immunosuppressive, neuroprotective, mostropic, neurole cantidiabetic, immunosuppressive, neuroprotective, mostropic, neurole cantidiabetic, orivicide, antidiathritic, antithyroid, thyrominm contropic, neurole cantidiabetic, antidoapalant, annostatic, antithyroid, thyrominm conversity, virucide, haemostatic, antithyroid, thyrominm conversity, antithyroid, thyrominm conversity, antithyroid, thyrominm conversity, antithyroid, anticonvuls, thrombolytic, anticoapalant, annostatic, antithyroid, antithyroid, thyrominm conversity, antithyroid, antithyroid, thyrominm conversity, antithyroid, anticonvuls, thrombolytic, anticoapalant, anticonvuls, antithyroid, antithyroid, thyrominm conversity, antithyroid, antithyroid, thyrominm conversity, antithyroid, antithyroid, antithyroid, antithyroid, antithyroid, associated with the expression of human molecules. In particular, thrombolyropenia, autoimmune/inflammatory disorders (e.g. arteriosclerosis, cancer, bracer, bracer, lung cancer, bracer, bracer, lung cancer, bracer, cervix cancer, both cancer, carver, disease, thyroiditis, multiple sclerosis, osteoarthritis, rheumator, alterosclerosis, hypopituitarism, hypopituitarism, hypopynadism, gigantism, goiter) metabolic, arthritis, scleroderma, systemic lupus erythematosus), infections (e.g. hypercholesterolaemia, hypoglycaemia, diabetes coriores (e.g. hypercholesterolaemia, hypoglycaemia, diabetes anxiety, schizophrenia), gastrointestinal disorders (e.g. ischaemic correbrovascular disease, stroke, Alzheimer's disease, pick's disease, crutifeldt-Jakob disease, correbrovascular disorders (e.g. akinesia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human diagnostic and therapeutic polynucleotides and polypep useful for diagnosing, treating or preventing e.g. leukemia, bra cancer, atherosclerosis, AIDS, thyroiditis, infections, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-636732/60.
P-PSDB; ADE31156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel isolated human diagnostic and therapeutic polynucleotide (designated dithp). The novel dithp polynucleotide comprises: any of 188 DNA sequences consisting observation polynucleotide comprises to the specification; a polynucleotide base pairs fully defined in the specification; a polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones AL, Dahl CR, Gietzen D, Chinn J, Dufour GB, Jackson J
Yu JY, Tuason O, Yap PE, Amshey SR, Dam TC, Liu TF, Gersti
Peralta CH, Lewis SA, Chen A, Marwaha R, Lan RY, Urashka ME
Kristnam SR, Kolluru V, Panesar IS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JAN-2002; 2002US-0349384P.
17-JAN-2002; 2002US-0349413P.
17-JAN-2002; 2002US-0349946P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 100; 634pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or Alzheimer's.
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  BP; 1105 A; 577 C;
601 G; 1075 T; 0 U; 0 Other;
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Alignment Scores:

2169 CCTTTGCATCTTTTCGTTTCACAGTATTTAATTTTATGACTCTAAAAAATATGTTTCTTT 2110	Db
54Leu 54	γQ
2229 GTATAGCATGTTTTATTCATTCAGGGGTTTTTTTGTTTTGTTAGTAATTTTCAATTTATTT	requences Db
53 53	Qy
2289 ATCATAAGGAACAGGGTTGTCTGCTTACCTGAATATCAGCTATAGTCTATATTTGCCAAA 2230	sease, Db
53 53	nic Qy
2349 CCAACCAATAGAAGAGCAAACATAGACAGGGGCAGTGATTGGCCTCTTATTGTTCGGGTC 2290	netabolic Db
53 53	disorders Qy
2409 ACAAGTTCTTATTATTGACGTTCATCATTAAGCAGTTATTGTCAACTTCAAGCCCATTTT 2350	neumatoid Db
53 53	Qy
2469 ATAGGAAACTACAACAACAACGACACGTGCTTCCCACAGTGAAATAATAGGAAGTATAGG 2410	erosis, Db
53 53	noma, brain Oy
2529 CAGACAGGGTCCCCCGCACCCCCTTTGTTTTAGAATACTACAGAGGCTACTGCCATAT 2470	
53 53	erapy and Oy
2589 TTAACATAAGGACATTAAAGATGCAATGCACAGAATTAAATCACACAATTACTTAC	onvulsant, Db
53 53	catic, Qy
2649 AGAACGTGCTTCGTAAACTAACATACTGCAAAAAAGGTAAAATAAGAGAAATATATAT	lipaemic, Db
53 53	nentioned Qy
2709 CATAAAGGCTGAAATAGTTTGCAGATACAGTTATGTATTTTGCCAAATAATGTATGT	nentary to
53 53	
2769 GTACACGAATTTATAATTCTTAGCCTTTCTTAATAAAATGGTAAGAGGTTCATATCTGTA 2710	05 195-7798 Db
53 53	Qy
2829 TITTATCTTAGTAAACTGAACACAAAATTCACATATGGTGAGAAAAAATAGAAAGCAGTA 2770	Дb
53 53	, stroke Qy
2889 TGTCCATTTCAACTAAGTAGCAATAGATGTGCTACCACCATTCACCTAAATATTTCTGAA 2830	ptides, Db
53 53	Qy
	Db
50 ProGlyAspMet 53	fB; Qy
TCAGATTTTCTGCTTCTTGGAAAGTC-TTGG	
30 LeuhlaLeuValGinGlyValSerAspPheLeuLeuGlyLysSerLeuAspIleAla 49	Qy
10 LeuThrAsnLysValGluPheProPheLeuValLeuLeuIleSerGlyGlyHisCysLeu 29 :::	Qy Db
US-10-649-273-2_COPY_148_414 (1-267) x ADE31345 (1-3358)	. Us-
Pred. No.:       2.99e-102       Length:       3358         Score:       995.50       Matches:       250         Percent Similarity:       44.82%       Conservative:       1         Best Local Similarity:       44.64%       Mismatches:       7         Query Match:       71.88%       Indels:       307         DB:       10       Gaps:       2	Pred. Score Perces Best J Query DB:

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RESULT 12
ABQ75508
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XX ABQ75
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 06-DEC-2000; 2000US-0251803P.
06-DEC-2000; 2000US-0251820P.
                                                                                                                                                          Murine; mouse; protease; calcium activated neutral protease type 5; CAPN5; tryptase 4; sialoglycoprotease; enzyme; genetic disease; caprological; neuropsychological; psychotic illness; transgenic animal;
                                        05-DEC-2001; 2001WO-US046405
                                                                    13-JUN-2002
                                                                                             WO200245491-A2
                                                                                                                       Mus musculus
                                                                                                                                                                                                               Murine sialoglycoprotease-like gene sequence SEQ ID NO:7.
                                                                                                                                                                                                                                              07-NOV-2002
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Novel transgenic animal, comprising a disruption in protease target gene, is useful for identifying agents that ameliorates a phenotype associated with a disruption in a protease target gene.
                                                                                                                                                        Example 3; Fig 7; 62pp; English.
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                                                                                                                                                                                                                           (DELT-) DELTAGEN INC.
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The present invention describes a non-human transgenic animal (I) C comprising a disruption in a protease target gene (PG) selected from CC calcium activated neutral protease type 5 (CAPN5) gene, tryptase 4 gene CC and sialoglycoprotease-like gene. Also described is a targeting construct (II), comprising a first polynucleotide sequence homologous to at least a CC first portion of PG, a second polynucleotide sequence homologous to at least a gene as a second portion of PG and a selectable marker. (II) is useful for CC producing a transgenic mouse comprising a disruption in a protease target CC gene, by introducing (II) into a cell, introducing the cell into a CC blastocyst, implanting the resulting blastocyst into a pseudopregnant CC gene, by repeated the pseudopregnant mouse gives birth to a chimeric mouse, and breeding the chimeric mouse to produce the transgenic mouse. (I) is CC useful for identifying an agent that modulates the expression or function CC useful for identifying an agent that modulates the expression or function CC target gene in (I) is modulated. (I) is also useful for testing the CC target gene in (I) is modulated. (I) is also useful for testing the CC genetic diseases, such as neurological, neuropsychological or psychotic illness. The present sequence represents murine sialoglycoprotease-like gene sequence, which is used in an example from the present invention

Sequence 1572 BP; 459 A; 337 Ç 340 G; 429 T; 0 U; 7 Other;

Best Local S Query Match:

Percent Similarity: Best Local Similarity:

2.67e-101 983.00 84.21% 78.95% 70.97%

Length:
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed
                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to asse
                                                                                                                                                                          Claim 1; SEQ ID NO
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC genes. (I) is useful in gene therapy techniques to restore normal CC activity of (II) or to treat disease states involving (II). (II) is CC useful for generating antibodies against it, detecting or quantitating a CC useful for generating antibodies against it, detecting or quantitating a CC polypeptide in tissue, as molecular weight markers and as a food CC supplement. (II) and its binding partners are useful in medical imaging CC is sites expressing (II). (I) and (II) are useful for treating disorders CC involving aberrant protein expression or biological activity. The CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC coding sequences. AAS64197-AAS94564 represent novel human diagnostic CC coding sequences of the invention. Note: The sequence data for this CC patent did not appear in the printed specification, but was obtained in CC electronic format directly from WIPO at CC ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2734 BP;
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 GACATAGAAGGCATCCGCTATGAACCAAAGTATGTGGCTCCTTCAGGGCTG
                   AspIleGluGlyIleArgTyrGluProLys-----CysProLeuGlyVal 247
                                                                    GGCATTATGAAATGCATGAATGGTATTGAAAGACTACGTGCTGGCTTGGGCATTTTACAT
                                                                                 GlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHis
                                                                                                                                                         LeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsn
                                                                                                                                                                                                                          ValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIle
                                                                                                                                                                                                                                                                                              ArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAla
                                                                                                                                                                                                                                                                                                                                                               SerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLys
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                                                                                                                                       TTAACAAACGCAACACAGTGCACTTTGTTGTGTCCTCCTCCCAGACTATGCACTGATAAT
                                                                                                                                                                                                                                                                            AGAACACATCGGGCTATTCTGTTTTGTAAGCAGAGAGACTTGTTACCTCAAAATAATGCA
                                                                                                                                                                                                                                                                                                                                             TCTTCAGCAGCAGACATTGCTGCCACAGTACAGCACAATGGCATGTCATCTTGTGAAA
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71.57%
66.50%
43.25%
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RESULT 14 ADL86725 ID ADL86 XX

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                                                                                                                                                                                                                                                                                                                                                                                                          self renewing multipotent progenitors (MPPB), common lymphoid progenitors (CLPB) and common myeloid progenitors (CMPB), which are collectively referred to as bone marrow stem cells populations. As such, these methods can be used to identify associated multi-lineage affiliated genes and hence the underlying molecular mechanisms in physiological haematopoietic development. This polynucleotide sequence is DNA associated with a murine MPP sub population of cells of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel method for predicting gene potential by associating nucleic acid sequences of unknown function with particular sub-population profiles. Specifically, it refers to classifying an unknown multi-lineage affiliated gene by collecting hybridisation data to develop a gene expression map, in order to determine the discrete sub-population where it is expressed. The present invention describes methods for predicting the lineage commitment of genes associated with the self-renewing haematopoietic (blood) stem cells (MSCs), as well as the non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Classifying an unknown multi-lineage affiliated gene comprises isolating expressed nucleic acid sequences from the discrete cell sub-populations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene potential; multi-lineage; cell commitment; haematopoietic stem cell; HSC; multipotent progenitor; MPP; common lymphoid progenitor; CLP; common myeloid progenitor; CMP; bone marrow stem cell; mouse; murine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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ThrGlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIle 216
                                             GCTATTCTGTTTTGCAAGCAGAGAAATTTGCTCTCCCAGCTAACGCAGTATTAGTTGTA
                                                                                                                                  AlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAla 176
                                                                                                                                                                      GACATTGCTGCTGCGGTACAGCATGCAACAGCGTGCCACCTTGCGAAAAGAACACATCGC
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Best Query Match:

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Percent Similarity:

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371 92 5 26

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                                        This invention relates to a novel method for predicting gene potential by associating nucleic acid sequences of unknown function with particular sub-population profiles. Specifically, it refers to classifying an unknown multi-lineage affiliated gene by collecting hybridisation data to develop a gene expression map, in order to determine the discrete sub-population where it is expressed. The present invention describes methods for predicting the lineage commitment of genes associated with the self-renewing haematopoietic (blood) stem cells (HSCs), as well as the nonself renewing multipotent progenitors (MPPB), common lymphoid progenitors (CLPs) and common myeloid progenitors (MPPB), which are collectively referred to as bone marrow stem cells populations. As such, these methods can be used to identify associated multi-lineage affiliated genes and hence the underlying molecular mechanisms in physiological haematopoietic development. This polymucleotide sequence is DNA associated with a murine
                                                                                                                                                                                                                                                                                                                                    Classifying an unknown expressed nucleic acid
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                             population of cells
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                                                                                                                                                                                                                                                                                                 3119; 123pp; English.
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US-10-649-273-2_COPY_148_414 (1-267) x ADL86726 (1-371)
Search completed: February 16, 2005, 13:58:48 Job time: 525.461 secs
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-Q=/Ggn2 1/USPTO spool/US10649273/runat 14022005 114704 16425/app query.fasta 1.1429
-DB=Issued Patenie NA -QPMT-fastap -SUPFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLGN=200 -THR SCORE-pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10649273 @CGN 1 1 292 @runat 14022005 114704 16425 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=30 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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                    US-09-774-528-177
US-10-067-443-23
US-10-067-443-21
US-10-067-443-21
US-10-067-443-20
US-09-596-002-38
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Sequence 177, App
Sequence 23, Appl
Sequence 1, Appli
Sequence 21, Appl
Sequence 20, Appl
Sequence 806, App
Sequence 806, App
Sequence 801, App
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Sequence 6612, App
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US-09-328-352-261 US-09-724-623-19	US-08-311-731A-131	US-09-692-570-1	US-08-916-421B-1	US-09-602-777A-147	US-09-103-840A-1	US-09-103-840A-2	US-08-781-986A-102	US-08-956-171E-102	US-09-438-185A-1	US-09-198-452A-1	US-09-221-017B-794	US-09-149-624-1	US-09-134-001C-1072	US-09-710-279-3985	US-09-134-000C-1551	US-09-710-279-727	US-09-790-988-1	US-09-107-433-1618	US-09-583-110-2196	US-09-066-512-1	US-08-961-527-214	-09	US-08-961-083-51	US-08-987-121A-3	US-08-987-121A-5	US-09-107-532A-2955	US-09-489-039A-2050	US-08-087-797-1	US-09-543-681A-2341	US-09-902-540-503
Sequence 261, App Sequence 19, Appl	٠,	, , ,	e 1	147,	۲,	e 2,	102,	102,	,,	Sequence 1, Appli	794,	Sequence 1, Appli	10	3985,	1551,	72	Sequence 1, Appli	Sequence 1618, Ap	Sequence 2196, Ap	Sequence 1, Appli	Sequence 214, App	Sequence 51, Appl	51	e 3,	æ	29	20	1, Ap	 23	Sequence 503, App

## ALIGNMENTS

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RESULT 1
US-09-774-528-177
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                                                                                                              PILE REFERENCE: 802
CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt FL genes Version 2.0
SEQ ID NO 177
SEQ ID NO 177
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           LENGTH: 1416
TYPE: DNA
ORGANISM: Homo s
FEATURE:
NAME/KEY: CDS
LOCATION: (205).
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TITLE OF INVENTION: No. 6743619el Nucleic Acids and TITLE OF INVENTION: Polypeptides
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Zhou, Ping
Zhou, Ch, Ryle
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Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
Wehrman, Tom
Wang, Jian-Rui
Wang, Dunrui
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Asundi, Vinod
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Sequence 23, Application US/10067443
Patent No. 6642041
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE
TITLE OF INVENTION: SPINAL CORD, MP-1
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                                                                                                 ProGlnLeuLysMetGluIle
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             EXPRESSED
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CURRENT PILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 1526
TYPE: DNA
ORGANISM: homo sapiens
US-10-067-443-23
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                                                AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr
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                       IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu
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Sequence 1, Application US/10067443

Patent No. 6642041

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED I

TITLE OF INVENTION: SPINAL CORD, MP-1

PILE REFERENCE: D0073 NP

CURRENT APPLICATION NUMBER: US/10/067,443

CURRENT FILING DATE: 2002-02-05

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR APPLICATION NUMBER: US 60/282,814

PRIOR PILING DATE: 2001-02-05

PRIOR PILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1

LENGTH: 2197
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DB:
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                                         GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla 140
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; LENGTH: 1387
; TYPE: DNA
; ORCANISM: homo sapiens
US-10-067-443-21
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Best Local Similarity:
Query Match:
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APPLICANT: Bristol-Weers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
NUMBER OF SEQ ID NOS: 71
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  LeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHis 80
                                                         LewiewGlyLyeSerLewAsp1leAlaFroGlyAspHetGeuAspLysValAlaArgArg
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Db 11744 TTTTGTTTTGTTAGTAATTTTCAATTTATTTCCTTTGCATCTTTTCGTTTCACAGTATTT 11803	7]	, ,
Qy 57 57	; ORGANISM: homo sapiens	! ~ . ~
Db 11684 TGAATATCAGCTATAGTCTATATTTGCCAAAGTATAGCATGTTTTATTCATTC		
Qy 57 57	TWARE: Pate	
Db 11624 GGGCAGTGATTGGCCTCTTATTGTTCGGGTCATCATAAGGAACAGGGTTGTCTGCTTACC 11683	PRIOR FILING DATE: 2001-04-10  NUMBER OF SEC ID NOS: 71	
Qy 57 57	PRIOR FILING DATE: 2001-02-00 5/200,310	
Db 11564 AAGCAGTTATTGTCAACTTCAAGCCCATTTTCCAACCAATAGAAGAGCAAACATAGACAG 11623	CURRENT FILING DATE: 2002-02-05 CURRENT FILING DATE: 2002-02-05 DETOR ADDITIONATION NITHERED. IIC 6/1/266 518	
Qy 57 57	FILE REFERENCE: D0073 NP  CIDERNY ADDITIONATION NIMPERS. HS/10/067 442	
Db 11504 CTTCCCACAGTGAAATAATAGGAAGTATAGGACAAGTTCTTATTATTGACGTTCATCATT 11563	FIGURE OF INTERVIOUS CONTROL OF THE PROPERTY O	
Qy 57 57	GENERAL INFORMATION:	.,
Db 11444 AATACTACAGAGGCTACTGCCATATATAGGAAAACAAACA	, Q 7	٠, ﺭ,
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Db 11324 GGTAAAATAAGAGAATATATATAGATTAACATAAGGACATTAAAGATGCAATGCACAGAA 11383	Db 1245 GGCATCCGCTATGAACCAAAATGTCCTCTTGGAGTAGACATATCAAAAAGAAGTTGGAGAA 1304	1
Qy . 57 57	Qy 236 GlylleArgTyrGluProLysCysProLeuGlyValAspIleSerLysGluValGlyGlu 255	2
Db 11264 TATTTTGCCAAATAATGTATGTGAAAGAACGTGCTTCGTAAACTAACATACTGCAAAAAA 11323	Db 1185 ATTGCATGGAATGGTATTGAAAGACTACGTGGTGGCTTGGGCATTTTACATGACATAGAA 1244	H
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Db 11204 AAATGGTAAGAGGTTCATATCTGTACATAAAGGCTGAAATAGTTTGCAGATACAGTTATG 11263	Db 1125 GCAACACAGTGCACTTTGTTGTGTCCTCCCAGACTATGCACTGATAATGGCATTATG 1184	ы
Qy 57 57	Qy 196 AlaThrGlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMet 215	0
11144 ATGGTGAGAAAAATAGAAAGAGTAGTACACAATTTTATAATTCTTAGCCTTTCTTAATA	1065 GCATCTGGTGGTGTCGCAAGTAACTTCTATATCCGCAGAGCTCTGGAAATTTTAACAAAC	ы
Qy 57 57	Qy 176 AlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsn 195	o
Db 11084 TACCACCATTCACCTAAATATTTCTGAATTTTATCTTAGTAAAACTGAAAAAAATTCACAT 11143	OY 156 ArgAlaiteLeurneCysLysGINAGASpLeuLeurCGINASNASNAIAValLeuVal 175 Db 1005 CGGGCTATTCTGTTAAGCAGAGAGACTTGTTACCTCAAAATAATGCAGTACTGGTT 1064	u ^
TTAATTTCTCCATTCTTTTTTGTTATGTTGTCCATTTCAACTAAGTAGCAATAGATGTGC	945 GCAGACATTGCTGCCACAGTACAGCACACAATGGCATGTCATCTTGTGAAAAGAACACAT	г
Qy 57 57	Qy 136 AlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHis 155	
Qy 41 LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysVal 57	Oy 127135	B C
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Qy 21 LeuLeulleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu 40	Qy 121 GlulysGluGluGlyIle 126	6
Qy 1 MetGluAlaHiBAlaLeuThrIleArgLeuThrAsnLyBValGluPheProPheLeuVal 20	Qy 101 AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys 120	2
US-10-649-273-2_COPY_148_414 (1-267) x US-10-067-443-20 (1-14364)	A 764	ы
Percent Similarity: 26.73% Conservative: 0  Best Local Similarity: 26.73% Mismatches: 2  Query Match: 59.53% Indels: 657  DB: 4 Gaps: 4	Db 645 CTTTCTTTAATAAACATCCAGAGTGCTCCACCATGAGTGGTGGGAAAGCCATAGAGCAT 704  Qy 81 LeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys 100	O D

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TANATGGTAGTAATTCATAGATGGAATTTTACATGGATATCAAAGAATAATTTTTTCAGA	TAGCTTCTATGGCACATAAGTCTAATTTTGCATCTTCTTGTTGGATTTAAAAGAGGGCTT 1252  174 ACAATAAAGAAAGTAAATGCAGTAACTGCTATCACTATTTTTAGAAAAATAAGAGGGCTT 1258  174 CCTTCATCCTTTGATGAAATCCCTTTGTTTGTTTGTTTTTAATAAGCCAGTCAAATTT 1264 AGCAGTGGGAGGTGGTATTCCAACTTTCGTGACAATGTTGTTTTTAATAAGCCAGTCAAATTT 1270 AGCAGTGGGAGGTGGTATTCCAACTTTCGTGACAATTTAAAAATTAAAGCCTTGACAAACTTT 1270 CACTATATTGTACCAGCCAAAATCCCTTTAAAATTAAAATTAAAACTAAAGTGGGAAAATGTT 1282 GTTTAACTGTATCTTAAAACTTTAAAAATTTATAAACTAAAGTGGGAAAATGTT 1282 GTTTAACTGTATCTTTAAAACTTTAAAAATTTATAAACTAAAGTGGGAAAATGTT 1282 174	124	65 LysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGln 84
Alignment Scores:  Pred. No.:  3.21e-20  Pred. No.:  308.50  Percent Similarity:  49.61*  Best Local Similarity:  31.98*  Mismatches:  Mismatches:  101  Query Match:  22.27*  Indels:  29	RESULT 6 US-09-596-002-38 ; Sequence 38, Application US/09596002 ; Patent No. 6632636 ; GEMERAL INFORMATION: APPLICANT: Patterson, Chandra APPLICANT: Patterson, Chandra APPLICANT: Berg, Kim, L. TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME FILE REFERENCE: PM-0008-4 US CURRENT APPLICATION NUMBER: US/09/596,002 ; CURRENT FILING DATE: 2000-06-16 FRIOR FILING DATE: 1999-06-18 NUMBER OF SEQ ID NOS: A1 SOPTWARE: SEQ ID NO 38 LENGTH: 94750 TYPE: DNA ORGANISM: M. catarrhalis FRATURE: NAME/KEY: misc_feature OTHER INFORMATION: Incyte template ID No. 6632636 38 PUBLICATION INFORMATION: US-09-596-002-38	CTGATATTTTCTCCAGGTTTAATTAGCAGCTTGGTTCATATCCATATATGATAGTTATT	Qy       174

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US-09-540-236-806
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                   NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 806
LENGTH: 1053
TYPE: DNA
ORGANISM: M.catarrhalis
                                                                                                                                                                                                                                                        Sequence 806, Application US/09540236 Patent No. 6673910
                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                         APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
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                                                                                                 GENERAL INFORMATION:
                                                                                                                 Sequence 884, Application US/09252991A Patent No. 6551795
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
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US-09-252-991A-884
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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 884
LENGTH: 1059
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                            GluproLysCysProLeu 245
                                                                                                                             CAGGTGTTCTACGCCCGCCCCCCCCTTCTGCACCGACAATGGCGCGATGATCGCCTACGCC 109
                                                                                      GlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyr 239
                                                                                                                                                   ThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsn 219
                                                                                                                                                                                                                            ValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCys 199
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CAGCCGCGCTGGCCGATG 40
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Best Local Similarity:
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SEQ ID NO 801
LENGTH: 1206
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Marc J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
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ValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCys 199
                                                                                                                                                                CTGGCGTTCCAGACCGCGGTGGTCGAGACCCTGCTGATCAAGTGCCGTCGCGCCTTG---
                                                                                                                                                                                                     AlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeu
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                                                                                                                                                                                                                                                                                                                                                                                                           CGCCTGGCGGAGCGCGCACTCCTGGCCGCTTCGTGTTCCCCGCGGCCGATGACCGATCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGATCGGCCTG---GGCTATCCC-------GGTGGTCCGGAAATCGCC 732
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                                                                                                                      PheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGly 179
                                                                                                                                                                                                                                               CGTTGCGTCGAGGCCGGCGACGACAGCGAGCAG-----ACCCGCTGCGACATCGCC
                                                                                                                                                                                                                                                                                                                            CCCGGCCTGGACTTCAGCTTCAGCGGGCTCAAGACCTTTACCCTGAAC---ACCTGGCAG
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291.50
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35.37%
21.05%
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Matches:
Conservative:
Mismatches:
Indels:
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DB:
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Best Local Similarity:
Query Match:
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Patent No. 6506581
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                            No . :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/557,884
PILING DATE: 25-Apr-2000
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
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CAGCCGCGCTGGCCGATG 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyr 239
                                                               ATGGAAGGGCATTTACTTGCGCCAATGCTTGATGACAATTCACCGCACTTTCCTTTTGTT
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COUNTRY: USA
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                                                                                                   MetGluAlaHisAlaLeuThrIleArgLeu---ThrAsnLysValGluPheProPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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US-09-643-990A-1/c
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                                                                                                                      ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
                       SOPTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Human G
                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                   STATE: MD
                                                                                                                                                                                                                                                                         CITY: Rockville,
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Hamilton O. Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Craig Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mark D.
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APPLICATION NUMBER: 08/487,429 FILING DATE: 1995-06-07

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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-649-273-2_COPY_148_414 (1-267) x US-09-643-990A-1 (1-1830121)
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SEQUENCE CHARACTERISTICS:
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FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELEPHONE: 301-610-5790
TELEPAX: 310-309-8439
552341 GGTGGCGAAGTGTTTTATCCTCAACCTCAATTTTGTÄCAGÄTÄÄTGGTGCGÄTGÄTTGCT 552282
                                                                                                                                                                                                                                                                                                                                                        552542 GCAATTAAAAACGAGGGGGAACTGATAGAGCAA----
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                                                                                                                                                                    ---ATTAAATGTAAG---CGTGCATTGAAAGAAACAGGCTATAAACGTTTAGTGATTGCG 552402
                      GlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAla 217
                                                                                                           GlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThr
                                                                                                                                                                                                          IleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSer 177
                                                                                                                                                                                                                                                                                                                                                                            LysGluLysGluGly------IleGluLysGlyGlnIleLeuSerSerAlaAlaAsp 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTTTTAGCGGAAAAAGGTACGCCAAATCGTTTCACATTTCCACGTCCAATGACAGATCGT 552603
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                    GGAGGGGTGAGCGCAAATAAAAAAACTCCGAGAAACGCTTGCGCACTTAATGCAAAATTTA 552342
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APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

FITLE OF INVENTION: Myxococcus xanthus Genome Sec FILE REFERENCE: 38-10 (15849) B.

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 6612

LENGTH: 996

TYPE: DNA

ORGANISM: Myxococcus xanthus

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                                                                                                                 136 AlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHis 155
                                                                                                                                                         646 GCGGTGCTGCACCACGTGCAGAAGCACGGCGTGCCGCAGGGGCAGGCGCTG------
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                                  ArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuVal 175
                                                                                                                                                                                                                                  GCGCTGCCGGGCGACAACTTCGACGTGTCCTTCTCCGGGTTGAAG
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                                                                                                                                                                                                                                                                                                                 CAGTTGGCGCAGCAGGGGAACCCCGGAGGCCATCCGCTTC
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  CTGGTGGCCGCCGCCGCTTG------GGCCACAAGCAGTTGGTG
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LENGTH: 2582
TYPE: DNA
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
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PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
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  AlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHis 155
                                             GCGGTGCTGCACCACGTGCAGAAGCACGGCGTGCCGCAGGGGCAGGCGCTG-----
                                                                                                                                                                 LeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLys 115
                                                                                                                                                                                                                CAGTTGGCGCAGCAGGGGAACCCGGAGGCCATCCGCTTC
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                                                                                   IleIleMetLysGysGluLysGluGlyIleGluLysGlyGlnIleLeuSerSerAla 135
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282.00
48.93%
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.1002-001 CURRENT APPLICATION NUMBER: US/09/543,681A CURRENT FILING DATE: 2000-04-05 PRIOR APPLICATION NUMBER: US 60/128,706 PRIOR APPLICATION NUMBER: US 60/128,706 PRIOR FILING DATE: 1999-04-09 NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 2341
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ORGANISM: Proteus
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664 CCCGGACTCGÁCTTTÁGTTTCTCTGGTTTAAAAAACCTTTTGCCGCTAATACTATTCGTCAA
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                              LysAsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLys 119
                                                                    HisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAla
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Patent No. 554331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Mellors, Alan
APPLICANT: Lo, Reggie Y.C.
APPLICANT: Abdullah, Khalid M.
TITLE OF INVENTION: Pasteurella Haemolytica
TITLE OF INVENTION: Glycoprotease
TITLE OF INVENTION: Gene and the Purified Enzyme
                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Layton, Jr., Samuel G.
REGISTRATION NUMBER: 22807
REFERENCE/DOCKET NUMBER: 3374-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 704 377 1561
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,797
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                              TELEFAX: 704 334 2014 INFORMATION FOR SEQ ID NO:
TOPOLOGY: 1ii
MCLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
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ADDRESSEE: Bell, Seltzer, Park & Gibson, P.A. STREET: 1211 Bast Morehead Street,
                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                        LENGTH: 1315 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                            TELEPHONE: 70% 2014
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STATE: No. 5543312th Carolina
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1080 GGCTTTCTTCGCTTAAAA 109
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                                    220 GlyIleGluArgLeuArg 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      534 GCATTATTGATTTCAGGTGGACACACCCAACTGGTAAAAGTTGACGGCGTTGGGCAATAC 593
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                                                                                                    ThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsn 219
                                                                                                                                                    GTAAGTGCCAATAAACAATTACGAGCAGACCTTGCGGAAATGAAAAAATTAAAAGGC 1019
                                                                                                                                                                                                                                                                     PheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGly 179
                                                                                                                                                                                                                                                                                                                                                                                        AATCTTAATGAAAATGGTGAACTCGATGAGCAA-----ACCAAATGCGATATTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATTAGCCGAATCCGGCACGCCAAATCGTTTTAAATTCCCTCGTCCAATGACCGACAGA 752
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Search completed: February 16, Job time : 1648.75 secs

2005, 22:15:40

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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-Q=/cgn2_1/USPTO_spool/US1649273/runat_14022005_114706_16497/app_query.fasta_1.1429
-DB=Published_Applications_NA_-OpmT=fastap_SUFFIX=rnpb_-MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=US10649273 @CCN 1 1 1053 @runat 14022005_114706_16497
-MAXIEN=200000000 -USER=US10649273 @CCN 1 1 1053 @runat 14022005_114706_16497
-NCPU=5 -ICPU=3 -NO_MAAP -LARGGUGERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1: /cgm2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgm2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgm2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgm2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

5: /cgm2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgm2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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                            / Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/ Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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/ Cgn2_6/ptodata/2/pubpna/US108_PUBCOMB.seq:*
/ Cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 9682, Ap Sequence 39301, A Sequence 41977, A Sequence 1920, A Sequence 2534, A Sequence 31809, A Sequence 6207, Ap Sequence 20511, A	7447, 20, 1 20, 1 20, 1 3118, 3118, 6641 1124, 815, 815, 815, 815, 815, 815, 815, 815	Description  Sequence 27, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 21, Appli Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 40, Appl

## ALIGNMENTS

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RESULT 1

US-10-120-988-177

Sequence 177, Application US/10120988

Publication No. US20030219745A1

GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Godrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Wang, Dunrui

APPLICANT: Wang, Dunrui

APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030219745A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 802CON

CURRENT APPLICATION NUMBER: US/10/120,988

CURRENT APPLICATION NUMBER: US/10/120,988

CURRENT PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: 09/774,528

PRIOR FILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 441

SOPTWARE: pt_FL_genes Version 2.0
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; NAME/KEY: CDS
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US-10-120-988-177
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ORGANISM: Homo sapiens
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ProGlnLeuLysMetGluIle 267
                                         ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal
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                                                                                                              IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu
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; LENGTH: 1526
; TYPE: DNA
; ORGANISM: homo s
US-10-067-443-23
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; Publication No. US20030082782A1
; ERNERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITITLB OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED :
TITLB OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: DO073 NP
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
; CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ 1D NOS: 71
; SOFTWARE: PatentIn version 3.0
; ENCOTION 0.23
; LENGTH 1.1526
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AlaSerAsnPheTyrIleArgAlgLeuGluIleLeuThrAsnAlaThrGlnCysThr
                                                                CysLysGlnArgAspLeuLeuProGlnAsnAlaValLeuValAlaSerGlyGlyVal
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CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 23
LENGTH: 1526
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Publication No. US20040043407A1
GENERAL INFORMATION:
APPLICANT: Bristcol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 CNT
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; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 60/266,518
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 10/067,443
; PRIOR APPLICATION NUMBER: US 10/067,443
; PRIOR FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/282,814
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 71
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Publication No. US20040048302A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  SEQ ID NO 23
LENGTH: 1526
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                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.2
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ORGANISM: homo
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Sequence 1, Application US/10067443

Publication No. US20030082782A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A N
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443

CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 2197
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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FILE REFERENCE: DOOT3 CNT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR RILING DATE: 2002-02-05
PRIOR RPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 1
LENGTH: 2197
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAMEX/KEY: CDS
LOCATION: (231)..(1472)
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE,
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TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
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Publication No. US20040048302A1
GENERAL INFORMATION:
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NAME/KEY: CDS
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                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0 SEQ ID NO 21 LENGTH: 1387
                                                                                                                                                                                                                                                                                                        APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
NUMBER: OF SEQ ID NOS: 71
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                                                                                                                                                            Sequence 21, Application US/10649273
Publication No. US20040043407A1
GENERAL INFORMATION:
                                                                               APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING
FILE REFERENCE: D0073 CNT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
 PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
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; PRIOR FILING DATE: 2001-04-10; NUMBER OF SEQ ID NOS: 71.; SOFTWARE: PATENTIN VERSION 3.2; SEQ ID NO 21; LENGTH: 1387; TYPE: DNA; ORGANISM: homo sapiens
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Best Local Similarity:
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Matches:
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Sequence 21, Application US/10651722

Publication No. US20040048302A1

GENERAL INFORMATION:

APPLICANT: Briscol-Myers Squibb Company

FILE REFERENCE: D0073 DIV

CURRENT APPLICATION NUMBER: US/10/651,722

CURRENT APPLICATION NUMBER: US 60/266,518

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR APPLICATION NUMBER: US 60/266,443

PRIOR APPLICATION NUMBER: US 10/067,443

PRIOR APPLICATION NUMBER: US 60/282,814

PRIOR APPLICATION NUMBER: US 50/282,814

PRIOR FILING DATE: 2001-02-05

PRIOR FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PatentIn version 3.2

SEQ ID NO 21

LENGTH: 1387

TYPE: DNA

ORGANISM: homo sapiens
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                                                                                                                              GluLysGluGluGlyIle------
                                                                                                                                                                      AlaSerIleLysValProGlnLeuLysMetGluIle 267
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leiby, Kevin R.
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
ITITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
ITITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND
ITITLE OF INVENTION: THEREOF
FILE REFERENCE: 381552004900
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 60/246,768
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR FILING DATE: 2000-11-15
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                                                                                                                                                                                                                            Alignment Scores:
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                                                                                                                   US-10-649-273-2_COPY_148_414 (1-267) x US-10-012-140-6 (1-1245)
                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                        US-10-012-140-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/10012140 Publication No. US20030009017A1
                                                                                                                                                                                                                                                                                                          SEQ ID NO 6
                                                                                                                                                                                                                                                                              LENGTH: 12
TYPE: DNA
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APPLICANT: Leiby, Kevin R.
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
ITILE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUM
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 381552004900
CURRENT APPLICATION NUMBER: US/10/012,140
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 60/246,768
PRIOR APPLICATION NUMBER: 60/246,768
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 49
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10012140 Publication No. US20030009017A1 GENERAL INFORMATION:
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ORGANISM: Homo FEATURE:

sapiens

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; NAME/KEY: CDS
; LOCATION: (146)...(1390)
; FEATURE:
; PANTE/KEY: misc_feature
; LOCATION: (1)...(1820)
; OTHER INFORMATION: n = A,T,C ox
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                                                                                                       IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu 240
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ProGlnLeuLysMetGluIle 267
                            ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal 260
                                                                                                                                                                                                                             AlaSerAsnPheTyrIleArgA1gAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr 200
                                                                                                                                                                                                                                                                                         CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal 180
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US-10-094-749-400
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DB:
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Best Local Similarity:
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APPLICANT: NAGAI, KEJICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: SOSHIKAMA, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NASUHO, YASUHIKO
TITLE OF INVENTION: NUMBER: US/10/094,749
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: G0/350,435
PRIOR FILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
PRIOR PELING DATE: 2001-09-14
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APPLICANT: SUGIYAM
APPLICANT: OTSUKI,
APPLICANT: WAKAMAT
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys 120
                                                   LeunlalycGlmGlynsmargFheHisFheAspIleLysFroProLeuHisHisAiaLys 100
                                                                                                                       LeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHis 80
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US-10-649-273-2_COPY_148_414 (1-267) x US-10-723-860-7447 (1-2890)  1 MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal 20	Alignment Scores: Pred. No.: 1.15e-145 Score: 1204.00 Percent Similarity: 89.51% Best Local Similarity: 89.51% Query Match: 18 Gaps: 1 2890 Matches: 239 Conservative: 0 Mismatches: 4 Gaps: 1 Gaps: 1	; ORGANISM: Homo sapiens ; FEATURE; ; NAME/KEY: misc feature ; LOCATION: (646)(657) ; OTHER INFORMATION: n is a, c, g, or t US-10-723-860-7447	SE C S	CURRENT APPLICATION NUMBER: US/10/723,860  CURRENT FILING DATE: 2003-11-26  PRIOR APPLICATION NUMBER: 60/429,739  PRIOR FILING DATE: 2002-11-26			RESULT 14 US-10-723-860-7447 ; Sequence 7447, Application US/10723860 : Publication US/10723860	Qy 261 ProGlnLeuLysMetGluIle 267	Cy 241 ProLysCysProLeuGiyValAspileSerLysGluValGlyGluAlaSerIleLysVal 260	1435	221 IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu	Qy 201 LeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGly 220	Qy 181 AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr 200	Qy 161 CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal 180	Qy 141 ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe 160	Qy 121 GluLysGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla 140	
; FRIOR ; NUMBER ; SOFTWA ; SEQ ID	; TITLE ( FILE RI ; CURRENY ; CURRENY ; PRIOR ; PRIOR ; PRIOR ; PRIOR ;	RESULT 15 US-10-067 ; Sequenc; ; Publicat ; GENERAL; ; APPLIC; ; APPLICS	Ody	B & £	B &	용 성	B. 8	B &	B &	Ф	Ş	B &	P Q	B 8	B &	B 8	₽
NUMBER OF SEQ ID NOS: 71  SOFTWARE: Patentin version 3.0  EQ ID NO 20	OF INVENTION: SPINAL CORD, MP-1 REFERENCE: D0073 NP VIT APPLICATION NUMBER: US/10/067,443 VIT FILING DATE: 2002-02-05 APPLICATION NUMBER: US 60/266,518 FILING DATE: 2001-02-05 APPLICATION NUMBER: US 60/282,814 WILLIAM DATE: 2001-04-10	SULT 15 -10-067-443-20 Sequence 20, Application US/10067443 Sequence 20, Application US/10067443 Publication No. US20030082782A1 GENERAL INFORMATION: APPLICANT: Bristol-Myers Squibb Company APPLICANT: Bristol-Myers Squibb Company TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED IN	261 ProGlnLeuLysMetGluIle 267                   2150 CCACAATTAAAAATGGAGATA 2170	ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal	221 IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu 240	201 LeuLeuCysProProProArgLeuCysThrAspAsnGJyIleMetIleAlaTrpAsnGJy 220 	181 AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr 200             1982 GCAAGTAACTTCTGTATCCGCAGAGCTCTGGAAATTTTAACAAACGCAACACGTGCACT 2041	161 CysiysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal 180 	141 ThrValG1nHsThrMetAlaCysHsaLeuVallysArgThrHsArgAlaIIeLeuPhe 160 	GAAAAAGGGAAGGTATTGAGAAGGGGCAAATCCTGTCTTCAGCAGCAGCACATTGCTGCC	GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla	101 AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys 120 	81 LeualalysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys 100 	61 LeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHis 80 	41 LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg 60 	21 LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu 40 	

Oy 57 57	Db 11624 GGGCAGTGATTGGCCTCTTATTGTTCGGGTCATCATAAGGAACAGGGTTGTCTGCTTACC 11683	Qy 57 57	Db 11564 AAGCAGTTATTGTCAACTTCAAGCCCATTTTCCAACCAATAGAAGAGCAAACATAGACAG 11623	Qy 57 57	Db 11504 CTTCCCACAGTGAAATAATAGGAAGTATAGGACAAGTTCTTATTATTGACGTTCATCATT 11563	Qy 57 57	Db 11444 AATACTACAGAGGCTACTGCCATATATAGGAAAAAAAAAA	Qy 57 57	11384 TTAAATCACAAATTACTTACACCACAGACAGGGTCCCCCCCC	57	СУ ). Т. 1.1.3.24 ССТВАВАНТАВСВСВАТАТАТАТАТАТАТСЯТТВАСАТТВАВСЕТТЕ В В СЕТТЕ В В СЕТТЕ В В СЕТТЕ В В СЕТТЕ В В	11264 TAFTTIGCCAAATAATGTATGTGAAAGAACGTGCTTCGTAAACTAACATACTGCAAAAAA 1	57	11204 AAATGGTAAGAGGTTCATATCTGTACATAAAGGCTGAAATAGTTTGCAGATACAGTTATG	Qy 57 57	Db 11144 ATGGTGAGAAAAATAGAAAGAGTAGTACACAATTTTATAATTCTTAGCCTTTCTTAATA 11203	Qy 57 57	Db . 11084 TACCACCATTCACCTAAATATTTCTGAATTTTATCTTAGTAAAACTGAAAAAAATTCACAT 11143	Qy 57 57	Db 11024 TTAATTTCTCCATTCTTTTTGTTATGTTGTCCATTTCAACTAAGTAGCAATAGATGTGC 11083	Qy 57 57	10965 CTTCATGGAAAGTCTTTGGACATAGCACCAGGTGACATGCTTGACAAGGT-AATTAAGAA	Qy 41 LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysVal 57	Db 10905 CTTTTGATTTCTGGAGGTCACTGTCTGTTGGCATTAGTTCAAGGAGTTTCAGATTTTCTG 10964	10895 AIGGAGGCICAIGCACIIACIAITAGGIIGACCAAIAAAGIAGAAITICCIITITITAGII 1	1 MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal 20	US-10-649-273-2_COPY_148_414 (1-267) x US-10-067-443-20 (1-14364)	59.53% Indels: 14 Gaps:	it Similarity: 26.73%	.84e-95 Length: 24.50 Matches:	-10-067-443-20	ORGANISM:
12764 GTTTAACTGTATCTTAAACTTTATTCATTTAAAAAATTATAAACTAAAGTGGGAAAATGTT	174	12704 CACTATATTGTACCACCCAAAATCCCTTTAATTGTGCTTAAAAGCCTTGAGAAAGATGGT	174	12644 AGCAGTGGGAGGTGGTATTCCAACTTTCGTGACACTAATGTTGATAAAGTTCTGATAATC	0v 174	1 70 2 7 「プログラス でんしょうしゅ でんしょうしょうしょうしょう マイ・ボール・ボール・ボール・ボール・ボール・ボール・ボール・ボール・ボール・ボール	00 174	176	12464 TAGCTTCTATGGCACATAAGTCTAATTTTGCATCTTCTTGTTGGATTTAAAAGAGGGCTT	Qy 174 174	Db 12404 GATAGGAAAGACTAACAGCCATTTCTTGTACTAGTTTGGTAGCTTTATGGGACAGCTGTA 12463	Qy 174 174	Db 12344 TGTTTAGGATGAACAGATCTTTATGCCTAGCCCTGACAGTATGAAATTATGCAG 12403	174	12284 ATTTTATAGTAATAGTTACACTTTGCAATATGTTACTTTTTTCCCAAGACCTTGACCTTG	174		יים יים ביים ביים ביים ביים ביים ביים ב		olofieffandoknoknokiitatokia kakknokokokokiitatoka pakadistitta pokadokiitatoka kakii a 1916.		12044 GGTATATTTCTAATTAGTAAAGTTGAACAGATAAATATTCCTGGATTGTGCCTAAAAATA	Qy 124 124 -	Db 11984 TCTTTTACTGGACTTCAACACGTTACTGATAAAAATAATGAAAAAAGGAAAAAGAGGAA 12043	Qy 105 SerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGlu 124	Db 11924 GGAAATAGATTTCATTTTGACATCAAACCTCCCTTGCATCATGCTAAAAATTGTGATTTT 11983	11864 AAACATCCAGAGTGCTCCACCATGAGTGGTGGGGGAAAGCCATAGAACATTTGGCCAAACAA	65 LysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGln 84	Db 11804 AATTTTATGACTCTAAAAAATATGTTTCTTTGATAGGTGGCAAGAAGACTTTCTTT	Qy 5864	Db 11744 TITTGTTTTGTTAGTAATTTTCAATTTATTTCCTTTGCATCTTTTCGTTTCACAGTATTT 11803	Qy 57 57

	CTGGCTTGGGCATTTTACATGACATAGAAGGCATCCGCTATGAACCAAAG 13533	13484	뮍
	laGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGluProLys 242	226	৪
13483	TGGAGCTATTGATTTTATTTTAATGCTTCTTATTTAGGAATGGTATTGAAAGACTACGTG	13424	밁
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13423	TCATAACTATGTAAATATTAATTGCCATTTTATCATACTAAGCCTTCTTCCTTC	13364	밝
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13363	ACTATGCACTGATAATGGCATTATGATTGCATGGTAAGCCACAGGATATACGTGCTTCAC	13304	뮍
218	9LeuCysThrAspAsnGlyIleMetIleAlaTrp	207	Ş
13303		13244	뮍
207	gArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProAr	187	Ş
13243		13184	₽
187	ValAlaSerGlyGlyValAlaSerAsnPheTyrIleAr	175	Ş
13183	CTGATATTTTTCTCCCAGGTTTAATTAGCAGCTTGGTTCATATCCATATATGATAGTTATT	13124	밁
174		174	S
13123	ATAGATATGTCATCTGCCCATTACCCATCTCAAAATGGGATAGTTTATTATTGTTTAATG 13123	13064	망
174		174	S
13063	AGTAATGTTTGTATGCTATTAGAATTATTAGTAATTTTTTTT	13004	뭥
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13003	TTGAAATTATATATAAATAATATTTAGATGAAAGGTTGGAAGAA	12944	D D
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12943	GTTATGTAGAAAATGCACAAAATAATAAAAATTTCAGGGTCTAAAATAGTGTACTATGA 12943	12884	망
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being print and is derived by analysis of the total score distribution.
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Match
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Listing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     first 45 summaries
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B85967
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QQECR6
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<b>4</b> 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
215.5	215.5	216	217	218	218	219	219.5	220	222.5	229.5	231	233	236.5	237.5	239.5
15.6	15.6	15.6	15.7	15.7	15.7	15.8	15.8	15.9	16.1	16.6	16.7	16.8	17.1	17.1	17.3
344	324	407	341	344	344	335	534	338	324	346	344	323	336	340	344
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
H70737	C71215	S50740	G89996	B86515	H72106	E81278	H69056	A71545	F75029	G86661	AB1705	G69388	E84936	B97011	AC1334
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probable o-sialogl	O-sialoglycoprote:	QRI7 protein - yea	hypothetical prote	O-sialoglycoprotei	o-sialoglycoprotei	probable glycoprot	O-sialoglycoprotei	probable o-sialogl	o-sialoglycoprotei	O-sialoglycoprotei	glycoprotein endop	O-sialoglycoprotei	O-sialoglycoprotei	probably O-sialogi	glycoprotein endop

## ALIGNMENTS

A; Title: Sequence and analysis of chromosome

sis of chromosome 2 of the plant Arabidopsis thaliana. MUID:20083487; PMID:10617197

A; Reference number: A84420; MUID:20083487; PMID:10617197 A; Accession: BE4888 A; Startus: preliminary A; Molecule type: DNA A; Residues: 1-463 <870> A; Cross-references: GB:AE002093; NID:92583127; PIDN:AAB82636.1; GSPDB:GN00139 C; Genetics: A; Genetics: A; Genetics: C; Superfamily: O-sialoglycoprotein endopeptidase C; Superfamily: O-sialoglyco	DPPPPATEPEDYVYDLRPRWPLGEEYAKGRSEA 436	Db 404
A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: E84888 A;Status: precliminary A;Molecule type: DNA A;Residues: 1-463 <sto> A;Residues: 1-463 <sto> A;Residues: 1-463 <sto> A;Residues: 1-463 <sto> A;Residues: 1-463 <sto> A;Residues: 1-463 <sto> A;Residues: 1-463 <sto> A;Residues: 1-463 <sto> A;Residues: 1-463 <sto> A;Residues: 1-463 <sto> A;Residues: 1-463 <sto> A;Residues: 1-463 <sto> A;Residues: 1-463 <sto> A;Residues: 1-463 <sto> A;Residues: 1-463 <residues: 1-463;re<="" 1-463;residues:="" td=""><td></td><td>240</td></residues:></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto></sto>		240
A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Recession: E84888 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-463 <5700- A;Residues: 1-463 <5700- A;Residues: 1-463 <5700- A;Genetics: A;Genetics: A;Genetics: C;Genetics: A;Gene: At2945270 A;Map position: 2 C;Superfamily: O-sialoglycoprotein endopeptidase  Query Match Best Local Similarity 36.6%; Score 409.5; DB 2; Length 463; Best Local Similarity 36.6%; Pred. No. 5.1e-29; Matches 100; Conservative 37; Mismatches 91; Indels 45; Gaps  Qy  1 MEAHALTIRLT-NKVEEPPFLVLLISGGHCLLALVQGVSDFLLIGKSLDIAPGDMLDKVAR 59	1	354
A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: E84888 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-463 <sto> A;Cross-references: GB:AE002093; NID:92583127; PIDN:AAB82636.1; GSPDB:GN00139 C;Genetics: A;Gene: A22945270 A;Map position: 2 C;Superfamily: O-sialoglycoprotein endopeptidase  Query Match Best Local Similarity 36.6%; Pred. No. 5.1e-29; Matches 100; Conservative 37; Mismatches 91; Indels 45; Gaps Matches 100; Conservative 37; Mismatches 91; Indels 45; Gaps  Qy  1 MEAHALTIRLT-NKVEFPPFLYLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVAR 59  </sto>	ASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRY 239	
A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: E84888 A;Scatus: preliminary A;Molecule type: DNA A;Residues: 1-463 <sto> A;Cross-references: GB:AE002093; NID:92583127; PIDN:AAB82636.1; GSPDB:GN00139 C;Genetics: A;Gene: At2945270 A;Map position: 2 C;Superfamily: O-sialoglycoprotein endopeptidase  Query Match Best Local Similarity 36.6%; Score 409.5; DB 2; Length 463; Best Local Similarity 36.6%; Pred. No. 5.1e-29; Matches 100; Conservative 37; Mismatches 91; Indels 45; Gaps 6  Qy  1 MEAHALTIRLT-NKVEFPFLVLLISGGHCILALVQGVSDFLLLGKSIDIAPGDMLDKVAR 59                                      </sto>	EIRNRADIAASFORVAVLHLEEKCERAIDWALELEPSIKHMVISGG 353	307
A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: E84888 A;Scatus: preliminary A;Molecule type: DNA A;Residues: 1-463 <5700> A;Residues: 1-463 <5700> A;Cross: references: GB:AE002093; NID:92583127; PIDN:AAB82636.1; GSPDB:GN00139 C;Genetics: A;Gene: At2945270 A;Map position: 2 C;Superfamily: O-sialoglycoprotein endopeptidase Query Match Best Local Similarity 36.6%; Score 409.5; DB 2; Length 463; Best Local Similarity 36.6%; Pred. No. 5.1e-29; Matches 100; Conservative 37; Mismatches 91; Indels 45; Gaps Matches 100; Conservative 37; Mismatches 91; Indels 45; Gaps Oy	EKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGG 179	120
A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: E84888 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-463 <sto> A;Cross-references: GB:AE002093; NID:92583127; PIDN:AAB82636.1; GSPDB:GN00139 C;Genetics: A;Gene: A72945270 A;Gene: A7294270 A;Gene: A72945270 A;Gene: A7294270 A;Gene: A72942</sto>	LGLDMHRSGGPAVEELALEGDAKSVKFNVPMKYHKDCNFSYAGLKTQVRLAIEA 306	252
A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: E84888 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-463 <5T00- A;Cross-references: GB:AE002093; NID:92583127; PIDN:AAB82636.1; GSPDB:GN00139 C;Genetics: A;Gene: At2945270 A;Map position: 2 C;Superfamily: O-sialoglycoprotein endopeptidase C;Superfamily: O-sialoglycoprotein endopeptidase Query Match Best Local Similarity 36.6%; Score 409.5; DB 2; Length 463; Best Local Similarity 36.6%; Pred. No. 5.1e-29; Matches 100; Conservative 37; Mismatches 91; Indels 45; Gaps Output MEAHALTIRLT-NKVEFPPTLYLLISGGHCLLALVQGVSDFLLIGKSLDIAPGDMLDKVAR 59	LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK 119	60
A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: E84888 A;Accession: B84888 A;Accession: Be4888 A;Accession: Braininary A;Molecule type: DNA A;Residues: 1-463 <5TO> A;Residues: 1-463 <5TO> A;Cross-references: GB:AE002093; NID:g2583127; PIDN:AAB82636.1; GSPDB:GN00139 C;Genetics: A;Gene: At2g45270 A;Map position: 2 C;Superfamily: O-sialoglycoprotein endopeptidase C;Superfamily: O-sialoglycoprotein endopeptidase C;Superfamily: O-sialoglycoprotein endopeptidase Query Match Best Local Similarity 36.6%; Pred. No. 5: 1e-29; Matches 100; Conservative 37; Mismatches 91; Indels 45; Gaps 6 Qy IMEAHALTIRLT-NKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVAR 59	EAHALVARLVEQELSFPFWALLISGGHNLLVLAHKLGQYTQLGTTVDDAIGEAFDKTAK 251	
A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: E84888 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-463 <sto> A;Cross-references: GB:AE002093; NID:92583127; PIDN:AAB82636.1; GSPDB:GN00139 C;Genetics: A;Gene: At2945270 A;Gene: At2945270 A;Gene: At2945270 A;Map position: 2 C;Superfamily: O-sialoglycoprotein endopeptidase C;Superfamily: O-sialoglycoprotein endopeptidase Apposition: 29.6%; Score 409.5; DB 2; Length 463; Best Local Similarity 36.6%; Pred. No. 5.1e-29; Matches 100; Conservative 37; Mismatches 91; Indels 45; Gaps 6</sto>	BAHALTIRLT-NKVBFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVAR 59	
A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: E84888 A;Accession: Bela88 A;Accession: Bela88 A;Cross-references: DNA A;Residues: 1-463 <sto> A;Cross-references: GB:AE002093; NID:g2583127; PIDN:AAB82636.1; GSPDB:GN00139 C;Gene: Access: GB:AE002093; NID:g2583127; PIDN:AAB82636.1; GSPDB:GN00139 C;Gene: Accession: 2 C;Superfamily: O-sialoglycoprotein endopeptidase</sto>	463; 45; Gaps	Query Match Best Local S Matches 100
A,Reference number: A84420; MUID:20083487; PMID:10617197 A,Accession: E84888 A,Status: preliminary A,Molecule type: DNA A,Residues: 1-463 <sto> A,Cross-references: GB:AE002093; NID:92583127; PIDN:AAB82636.1; GSPDB:GN00139 C;Genetics: A:22945270 A,Gene: At2945270 A,Map position: 2</sto>	O-sialoglycoprotein endopeptidase	C; Superfamily:
A,Reference number: A84420; MUID:20083487; PMID:10617197 A,Accession: E84888 A,Status: preliminary A,Molecule type: DNA A,Residues: 1-463 <sto> A,Cross-references: GB:AE002093; NID:92583127; PIDN:AAB82636.1; GSPDB:GN00139 C,Genetics:</sto>	2	A;Gene: AC2945 A;Map position
A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: B84888 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-463 <sto> A;Cross-references: GB:AE002093; NID:g2583127; PIDN:AAB82636.1; GSPDB:GN00139</sto>		C; Genetics:
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A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: B84888 A;Status: preliminary A.Molecule type: DNA A.Molecule type: DNA	63 <sto></sto>	A; Residues: 1-
A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: E84888	minary : DNA	A;Status: prel A;Molecule typ
A;Reference number: A84420; MUID:20083487; PMID:10617197	45 - 00 00 00	A; Accession: E
	ber: A84420; MUID:20083487; PMID:10617197	A; Reference nu

RESULT 2
AB2902
O-sialoglycoprotein endopeptidase gcp [imported] C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002

#text\_change 18-Nov-2002

Agrobacterium tumefaciens (strain C58

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C;Accession: AB2902
R;Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, R;Mood, D.W.; Setubal, J.C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, Perage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, Perage, S.; Karp, P.; Romero, P.; Zhang, S.; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Go:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Goodner, B.; Hinkle, G.; Gattung, A.; Liu, F.; Wollam, C.; Allinger, Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable o-sialoglycoprotein endopeptidase (glycoproteinase) [imported] - AcC;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: D97677
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                                                                                                                                                                                                 A; Gene: AGR C 4806
A; Map position: cii
C; Superfamily: O-si
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A;Residues: 1-366 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK88373.1; PID:g15157858; GSPDB:GN00169
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tun
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: D97677
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A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: gcp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-365 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
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C; Superfamily: (
                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
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                                                                                                Query Match
Best Local S
Matches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Map position: circular chromosome Superfamily: O-sialoglycoprotein endopeptidase
                                                                                                                                                                                               Superfamily: O-sialoglycoprotein endopeptidase
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Best Local :
     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGL----QHVTDKI
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                                                                                                                       Similarity
                         MEAHALTIRLTNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDI
LEGHALTARLTDGLSFPYLMLLVSGGHTQLVLVRGVGEYERWGTTIDDALGEAFDKTAKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APLSEQD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGL-PYP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGIRYEPKCPLGVDISKE 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVAGGVAANQETRQTLQALCDTHGFRFVAPPHRLCTDNAAMTAWAGLERMAEG----RQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNA--VL
                                                                                                                                                                                                                           circular chromosome
                                                                                                   Conservative
                                                                                                                     24.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----IADICASFQKAVSRTLKDRIGRGLARFKVE--FPHINGEPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GGPAVENAAAKGDPDRFPLPRPMVGEARLDFSFSGLKTAVRQAATAI
                                                                                              40;
                                                                                                                     Score 338; DB 2;
Pred. No. 1.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.; Miller, N.; Blanchard, M.; Qurollo, B.; Gold M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
                                                                                                   Mismatches
                                                                                                                                            Length 366
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [imported] - Agrobacterium
                                                                                              30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
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                                                                                              Gaps
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  180
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                                                                                                                O-sialoglycoprotein endopeptidase (EC 3.4.24.57) [imported] - Brucella melicipspecies: Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
                    C;Accession: AB3274
R;Dell'ecchio, V.G.; Kapatral, V.; Redkar, R.J.;
; Mazur, M.; Goltsman, B.; Selkov, B.; Elzer,
proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: E71711
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
Nature 396, 133-140, 1998
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C;Superfamily: O-s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable o-sialoglycoprotein endopeptidase (gcp) RP037 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-387 <AND>
                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: O-sialoglycoprotein endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                     Local
                                  196
                                                                    278 LKSFRKDEFNWKPLECITRPKYRIHIQNSYRSNLLNDTIVIAGGVAANKYLQEILSDCTR 337
                                                                                                         164
                                                                                                                                                                                  120
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                                                                                                                                                                                                                                                                                             113 LEGHALTARLTDNISYPYLLLLASGGHCQFVAVLGLGKYKILGTTIDDAVGETFDKVAKM 172
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                                                                                                                                                                                                                                                                                                                                1 MEAHALTIRLTNKVEFFFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR
                                                                                                                                                                                                                                                                                                                                                                      l Similarity
87; Conserv
                                                                                                                                                                                                                                                         LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APLSEQD------IADICASFQKAVSRTLKDRIGRGLARFKVE--FPHINGEPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNA--VL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGL----QHVTDKI
PYGYRLIAPPMHLCTDNAAMIAYAGLER
                                ATQCTLLCPPPRLCTDNGIMIAWNGIER
                                                                                                                                         KEVNDSV-----INDIAASFOFTIGAILSSKMQDAIRLYKQILNDYYEDINHPTKLN 277
                                                                                                                                                                            KEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQ----------
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                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                      -SPPGGPETEKRAKLGNPHKYKFPKPTINSGNCNMSFSGLKTAVRTLIMNL
                                                                                                                                                                                                                                                                                                                                                                  24.4%; Score 338; DB 2; 32.5%; Pred. No. 1.1e-22; ative 38; Mismatches 83
                                                                                                         -LLPQN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prowazekii and the origin of mitochondria PMID:9823893
365
                                  223
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                                                                                                         -NAVLVASGGVASNFYIRRALEILTN 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB:AJ235269;
                                                                                                                                                                                                                                                                                                                                                                      83;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 387;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NID: 93860572; PIDN: CAA14508
                                                                                                                                                                                                                                                                                                                                                                      60;
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                      225
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The genome sequence of the facultative intracellular pathogen Brucella melitensi

R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, lzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes

Letesso

Brucella melitensis

(strain

Hagius,

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A;Reference number: AD325
A;Accession: AB3274
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-359 (KUR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: E97707
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E97707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
C;Accession: E97707
                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: O-sialoglycoprotein endopeptidase C;Keywords: hydrolase; metalloproteinase
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C;Superfamily: O-sialoglycoprotein endopeptidase
C;Keywords: hydrolase; metalloproteinase
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A;Cross-references: GB:AE006914; PIDN:AAL02599.1; PID:g15619097; GSPDB:GN00173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O-sialoglycoprotein endopeptidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE008917; PIDN:AAL51357.1; PID:g17982056; GSPDB:GN00190
                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 81
                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
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Best Local Similarity
                                    179
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                                                                      226
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                                                                                                                                              LNL-----AFPGGPEIEKRAKLGDPHKYKFPKPIINSGNCNMSFSGLKTAVRTLIMTL 225
                                                                                                                                                                                                                     LEGHALTARLTDNIPYPYLLLLASGGHCQFVAVLGLGKYKILGSTIDDAVGBAFDKVAKM 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VASGGVASNFYIRRALBILTNATQCTLLCPPPRLCTDNGIMIAWNGIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPLTDQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGL-----QHVTDK 115
                                                                                                                                                                                  LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK- 119
                                                                                                                                                                                                                                                       MEAHALTIRLTNKVEFFFLVILISGGHCLLALVQGVSDFLLLGKSLDIAFGDMLDKVARR 60
 GVAANKYLOKILSSCAKTYGYRLIYPPIHLCTDNAAMIAYAGLER 320
                                  GVASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIER 223
                                                                      KBINDTV-----INDIAASFQFTIGEILSSKVQDAIRAYEQITNNFDKKN--IVIAG
                                                                                                    KEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQ-RDLLPQNNAVLVASG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVAGGVAANKTLRAALENLCTRHGFAFIAPPLNLCTDNAAMIAWAGAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGL-PYP-----GGPAVERMALOGDOKRFALPRPLKGEARLDFSFSGLKTAVRQTATEL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                             23.8%; Score 329.5; DB 2; ilarity 36.0%; Pred. No. 5.8e-22; Conservative 40; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AD3252; PMID:11756688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 334.5; DB 2
Pred. No. 2.2e-22;
33; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EC 3.4.24.57) [imported] - Rickettsia conorii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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R;Stover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                              A; Gene: gcp; P/C; Superfamily:
                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-341 <570>
A;Cross-references: GB:AE004494; GB:AE004091; NID:g9946446; PIDN:AAG03969.1;
                                                                                                                                                                                                                                                                                                                                       A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: H83572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O-sialoglycoprotein endopeptidase PA0580 [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa . C;Dsecies: Pseudomonas aeruginosa . C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: H83572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: CC0071
C;Superfamily: O-sialoglycoprotein endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.f. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hatt, D.H.; Kolona, D.J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: P87257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptidase M22 family protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
                                                                                                                                                                        C;Genetics:
                                                                                                                                                                                               A; Experimental source: strain
                                                                                                                                                                                                                                                                                                             A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-367 <STO>
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Query Match 21.0%; Score 291.5; DB 2
Best Local Similarity 35.4%; Pred. No. 1.5e-18;
Matches 87; Conservative 37; Mismatches 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 LEGHAVSARLGADIAYPPLLLLVSGGHCQLLEVSGVGACKRLGTTIDDAAGEAFDKIAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKK 120
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                                                                                                                                              PA0580
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                                                                                                           O-sialoglycoprotein endopeptidase
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K.; Lim,
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Indels

23;

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O-sialoglycoprotein endopeptidase (EC 3.4.24.57) - Haemophilus influenzae (strain N;Alternate names: sialoglycoproteinase (C;Species: Haemophilus influenzae
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C;Superfamily: O-sialoglycoprotein endopeptidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sialoglycoproteinase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: G70369
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A;Experimental source: strain VF5
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A; Residues: 1-335 < AQF >
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V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; nucleic acid sequence not shown; translation not
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                                                                                                                                                                                                            ASNFYIRRALEILTNATQ---CTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGI
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                                                                                                                          --QPNIPL 327
                                                                                                                                                          RYEPKCPL 245
                                                                                                                                                                                          SANSRLR---EVFKKASQEYGFELYIPHPSLSTDNALMIAYAGMERFKRGVVAPLDVNP-
                                                                                                                                                                                                                                                                                            EKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGV 180
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                                                                                                                                                                                                                                                             KKEKNVRK-----EDIAYSFQETVVEILLEKS----LWAMKKTGIKR---
                                                                                                                                                                                                                                                                                                                               LGL-GYP-----GGPIIDRLAKEGKKL-YPLPKPLMEEGNLNFSFSGLK---TAILNLL
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ilarity 34.3%;
Conservative 4
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; Pred. No. 1.8e-18;
46; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
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C;Accession: AI0079

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360
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AI0079
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C.Accession: H64074
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.F.; Kerlavage, R;Fleischmann, R.D.; Adams, M.D.; Whitey, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Fuhrmann, J.L.; Geoghagen, N.S.M., D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M., Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Commo
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C;Superfamily: O-sialoglycoprotein endopeptidase
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
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                                KEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNN-AVLVASG 178
                                                                                                                                                                                                                            RLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK 119
                                                                                                                                                                                                                                                                                                                     MEGHLLAPMLEENAPEFPFVALLVSGGHTQLISVTGIGEYLLLGESVDDAAGEAFDKTAK 171
                                                                                                                                                                                                                                                                                                                                                               MEAHALTIRL-TNKVEFPFLYLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVAR
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                                                                                                                                        -GGPMLSRMAQQGTVGRFTFPRPMTDRPGLDFSFSGLKTFAANTIRA 224
<u>:</u>
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Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelto A;Title: Complete genome sequence of a multiple drug resistant Salmon A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AG0892

A;Status: preliminary A;Molecule type: DNA

A;Residues: 1-337 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07733.1; PID:g16504285; GSPI C;Genetics: A;Gene: STY3387

C;Superfamily: O-sialoglycoprotein endopeptidase
                                                                                                                       C; Accession R; Hayashi,
                                                                                      C;Accession: C91122
R;Hayashi, T.; Makino, K.; Ohnishi,
gasawara, N.; Yasunaga, T.; Kuhara,
DNA Res. 8, 11-22, 2001
                A;Reference number: A99629;
A;Accession: C91122
A;Status: preliminary
                                                                                                                                                         probable O-sialoglycoprotein endopeptidase [imported] - Escherichia coli (strain
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable glycoprotease [imported] - Salmonella enterica subsp. enterica serovar CySpecies: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AG0892
                                                     A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Rcfcrcnce number: A39629; MUID:21156231; PMID:11258796
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 20.2%; Score 279.5; DB 2; Similarity 32.9%; Pred. No. 1.8e-17; 81; Conservative 35; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                 VASNEYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEGHILAPMLEDNPPDFPFVALLVSGGHTQLISVTGIGQYELLGESIDDAAGEAFDKTAK 171
                                                                                                                                                                                                                                                                                                                           EPKCPL
                                                                                                                                                                                                                                                                                                                                                            VSANRTLRAKLAEMMQKRRGEVFYARPEFCTDNGAMIAYAGMVRFKA--GVTADL-GVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                   QTRADIARAFEDAVVDTL-
                                                   MUID: 21156231;
                                                                                                       M.; Kurokawa, K.; Ishii, S.; Shiba, T.; Hattori,
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Shinagawa,
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probable O-sialoglycoprotein endopeptidase ygjD [imported] - Escherichia coli C;Species: Escherichia coli C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Date: 10-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: B85967
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D. iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K. Mature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:BA000007; PIDN:BAB37370.1; PID:g13363420; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE005174; NID:g12517643; PIDN:AAG58198.1; GSPDB:GN00145; UWGP:Z44JA;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: EC83947
C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-337 <STO>
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Matches
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Superfamily:
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Best Local Similarity
Matches 82; Conserv
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VSANTTLRAKLAEMYKKRRGEVFYARPEFCTDNGAMIAYAGMVRFKA-
                             VASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRY 239
                                                                                                                                                                                                                        RLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK 119
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                                                                                      --RDNGTDD----QTRADIARAFEDAVVDTLMIKCKRAL-----DLTGFKR--LVMAGG
                                                                                                                                    KEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --RDNGTDD----QTRADIARAFEDAVVDTLMIKCKRAL-----DLTGFKR--LVMAGG
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                                                                                                                                                                               -GGPLLSKMAAQGTAGREVEPREMTDRPGLDESESGLKTFAANTI--
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Pred. No. 2.2e-17;
36; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                          Mismatches 101;
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Apodaca,
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240 BPKCPL 245

326 RPRWPL 331

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A;Residues: 1-421 <WIL>
A;Cross-references: EMBL:Z81030; PIDN:CAB02716.1; GSPDB:GN00023; CESP:C01G10.10
A;Experimental source: clone C01G10
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein C01G10.10 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000 C;Accession: T18825 R;Matthews, L.
Search completed: February 16, 2005, 13:09:22 Job time: 14.1891 secs
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A;Map position: 5

A;Introns: 31/2; 72/3; 122/2; 177/1; 272/3; 315/1; 353/2
C;Superfamily: O-sialoglycoprotein endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, October 1996
A;Reference number: Z19027
A;Accession: T18825
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 19.9%; Score 276; DB 2; Length 421; Best Local Similarity 30.4%; Pred. No. 5e-17; Matches 85; Conservative 52; Mismatches 107; Indels 36; Gaps
                                                                                                              357
                                                                                                                                                                                                                                                                                177
                                                                                                                                                               237 IRYEP------KCPLGVDISKEVGEASIKVPQLKM 265
                                                                                                                                                                                                                         303 GGGVAANQYIFGAISKLSAAHNVTTIKVLLSLCTDNAEMIAYSGL-----LMLVNRSBA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                             194 OLGDL-GSEFDGIHVGAAVEILASRASADGHLRYPIFLPNVPKANWNFDQIKGSYLNLLE 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 MRAHALSILLVDDSVRFPFSAVLLSGGHALISVABDVEKFKLYGQSVGGSPGECIDKVAR 193
                                                                                                                                                                                                                                                                                                                                    253 RIRKNSETSID-----IPDFCASLONTVARHISSKLHIFFESLSEQEKLPKQ---LVI 302
                                                                                                                                                                                                                                                                                                                                                                                         117 IMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 RLSLIKHPECSTMSGGKAIEHLAKQGN---RFHFDIKPFLHHAKNCDFSFTGLQHVTDKI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEAHALTIRLT-NKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVAR 59
                                                                                                           IWWRPNDIPDTIYAHARSDIGTDASSEI----IDTPRRKL 392
                                                                                                                                                                                                                                                                          SGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEG 236
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Command line parameters:

-MODEL-frame+ p2n.mod(1) -DEV=Xlh
-MODEL-frame+ p2n.mod(1) -DEV=Xlh
-Q-/cgm2 1/USPTO_spool/US10649273/runat 14022005 114703 16411/app_query.fasta_1.1429
-DB=EST -QFMT=fastap -SUPFIX=Fst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human10.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=200000000
-USER-US10649273 @CGN 1 1 6799 @runat 14022005 114703 16411 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -KGAPOP=10 -KGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                      Result
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Maximum DB
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Maximum Match 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                      No.
                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                     Score
                                  1263
1224
1216
1097
1075
1071
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seq length: 2000000000
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                                                                                                                                                                                      Match
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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## ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL RESULT 1 BQ423651 LOCUS COMMENT FEATURES DEFINITION BQ423651 870. AGENCOURT 7790948 NIH\_MGC\_72 5', mRNA sequence. BQ423651 BQ423651.1 GI:21118966 1 (bases 1 to 870) National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov plate: LLAM13342 row: 1 column: 21 Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC/DCTD/DTP Homo sapiens (human) quality sequence stop: /mol\_type="mRNA" /db\_xref="taxon:9606" organism="Homo sapiens" ocation/Qualifiers clone="IMAGE:6065828" bp mRNA linear column 2018:6065828 linear EST 23-MAY-2002 þe

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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
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                                               Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 210-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
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Functional annotation of a full-length mouse
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Please visit our web site for further details.
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                                                                                  TTGGCCAAAGACGGAAATAGATTCCATTTTACTATCAATCCACCTATGCAGAATGCTAAG
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/db_xref="G1:26337529"
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/tanalation="mukHrRTNAAIPKPKPKSKVYGFLRRFSVHPRTLSCHKLVLGIET
SCDDTGAAVVDETGNVLGEALHSQTQVHLKTGGIVPVAQQLHRENIQRIVEETLSAC
RITPSDLSAIATTIKPGLALSLGVGLSFSLQLVNQPKKPFIPHHMEAHALTIRLTNK
VEFPFLVLLISGGHCLLALVQGVSBFLLLGKSLDIAPGDMLDKVARELSLIKHPEGSI
MSGGKAIEQLAKDGNRFHFTINPFMQNAKNCDFSFTGLQHITDKLITHKEKBEGIEKG
QILSSAADIAANQHATACHLAKRTHAAILFCKQKNLLSPANALVLVVSGGVASNLYIR
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                                   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., Oikazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y., Direning pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                       Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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High-efficiency full-length cDNA cloning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
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6 (bases 1 to 1622)
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Functional annotation of a full-length mouse cDNA collection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please visit our web site (http://genome.gsc.riken.jp/)
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/codon_start=1
/protein_id="Bab27506.1"
/protein_id="Bab27506.1"
/db_xref="GI:12847276"
/db_xref="GI:12847276"
/translation="MLMLRRTHAGAIPKPPKSKYYGFLRRESVHPRTLSCHKLYLGIETSCDDTGAAVVDETGNVLGEALHSQTQVHLKTGGIVPPVAQQLHRENIQRIVEETLSAC RITPSDLSALATIKPECLALSLGVGLSFSLQLVNQFKKPFIPHMENHALTIRLTNK VEFPFLVLLISGGHCLLALVQGYSDFLLLGKSLDIAPGDMLDKVARKLSLIKHPECST MSGGKALEQLAXOGNERHFTINPPMQNAKNCDFSFTGLQHITDKLITHKEKEEGIEKE GILSSAADIAAAVQHATACHLAKRTHRAILFCKQKNLLSPANAVLVVSGGVASNLYIR KALEIVANATOCTLLCPPRRLCTDNGIMIAMNGIERLRAGLGVLHDVEDIRYEPKCFL
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similar to PUTATIVE SIALOGLYCOPROTEASE TYPE 2 [Homo
sapiens] (SPTR|Q9H4B0, evidence: FASTY, 80%ID, 100%length,
                                                                                                                                                                                                                                                                                                                      /tissue_type="whole body"
/clone_lib="RIKEN full-length enriched mouse
/dev_stage="10 days embryo"
207. .1451
                                                                                                                                                                                                                                   match=1242) "
                                                                                                                                                                                                                                                                                                                                                                                                             clone="2610001M19"
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/strain="C57BL/6J"
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1 (bases 1 to 640)

Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,

Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

Expressed sequence tag analysis of human retina for the NEIBank project: Retbindin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts

Mol. Vis. 8 (4), 196-204 (2002)
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Plate: 03 row: d column: 11
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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hd03d11 y1 Human Retina
Homo sapiens cDNA clone
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Fax: 301 496 0078
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Section on Molecular Structure and Function
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                           GluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHis 98
  GAACATTTGGCCAAACAAGGAAATAGATTTCATTTTGACATCAAACCTCCCTTGCATCAT 122
                                                                                        AGAAGACTTTCTTTAATAAAACATCCAGAGTGCTCCACCATGAGTGGTGGGAAAGCCATA
                                                                                                               ArgArgLeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib."Human Retina cDNA (Un-normalized, unamplified): hd/he"
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bloserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strand synthesis was carried out using a Not I
                                                                                                                                                                                                                                                                                                                                                                                                                          [5'-pGACTAGTTCTAGATCGCGAGCGGCCGCC(T)15-3']. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer-adapter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hd03d11"
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1097.00
100.00%
100.00%
79.21%
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                          alternative
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REFERENCE
AUTHORS
TITLE
JOURNAL
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                                                                                    Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization

LU Unpublished (2001)

On May 13, 2003 this sequence version replaced gi:30611736.

Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-ligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and Cloned
into the Not I and EcoR V sites of the pCMVSPRT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BX391919 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens CDNA Clone CS0DK001YE02 3-PRIME, mRNA sequence.

BX391919
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; (bases 1 to 852)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX391919.2 GI:46846154
EST.
                                  For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAIO35ZEO7_CSO3317_1&c=1240.r
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATGAACCAAAATGTCCTCTTGGAGTAGACATATCAAAAGAAGTTGGAGAAGCTTCCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrGluProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATGGTATTGAAAGACTACGTGCTTGGCTTGGGCATTTTACATGACATAGAAGGCATCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTGTCGCAAGTAACTTCTATATCCGCAGAGCTCTGGAAATTTTAACAAACGCAACACAG
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Location/Qualifiers
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/organism="Homo sapiens"
/mol\_type="mRNA"
/db\_xref="taxon:9606"
/clone="CSODK001YE02"

ORIGIN

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RESULT 6
BC030671
     SOURCE
ORGANISM
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Best Local Similarity:
                                         KEYWORDS
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                                                                                                                DEFINITION
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                                         BC030671.1
HTC.
                                                                                           Mus musculus O-sialoglycoprotein clone IMAGE:1226118), containing
                                                                                                                                 BC030671
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     musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="Homo sapiens HELA CELLS COT 25-NORMALIZED" /note="Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
                                                         GI:21040459
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Conservative:
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frame-shift errors.
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COMMENT
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PUBMED
REFERENCE
US-10-649-273-2_COPY_148_414 (1-267)
                                                                                                            Score:
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Glbbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Wadan, A., Kodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schmerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Parally S. 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 66 Row: e Column: 10

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312463
This clone has the following problem: frame shifted.

Location/Qualifiers
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Tissue Procurement: Marcello Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
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Submitted (20-MAY-2002) National Institutes of Health, Mammalian Submitted (20-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA bequencing ...
http://www.systemsbiology.org
contact: amadanosystemsbiology.org
contact: amadanosystemsbiology.org
Anup Madan, Jessica Fahey, Brin Helton, Mark Ketteman, Anuradha
Anup Madan, Jessica Fahey, Brin Helton, Mark Ketteman, Anuradha
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/tissue_type="Thymus_gland, mouse"
/clone_lib="soares_thymus_2NbMT"
/lab_host="DH10B"
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            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 701)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                             BE740611
BE740611.1 GI:10154603
EST.
                                                                                                                                                                                                                 601595739F1 NIH_MGC_9
   Unpublished (1999)
                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                mRNA sequence.
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High quality sequence stop: 701.
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Tissue Procurement: DCTD/DTP
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heCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyV
                                                   laThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuP
                                                                                                                            GGAAACAAGAGGAAGGTATTGAGAAGGGGCAAATCCTGTCTTCAGCAGCAGACATTGCTG
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                                                                                                                                                                                                                    AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLys--L
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/db xref="taxxx:"
/db xref="taxxx:"
/clone="IMAGE:3949640"
/tissue_type="adenocarcinoma cell line"
/tissue_type="adenocarcinoma cell line"
/tissue_type="adenocarcinoma cell line"
/tissue_type="adenocarcinoma cell line"
/tome=IbH10B (phage=resistant)"
/clone=lib="NIH_MGC_9"
/clone="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2:
/note="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2:
/coned into EccRI/KhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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|mol_type="mRNA"
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TITLE
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2603 row: d column: 15
High quality sequence stop: 584.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLLett. CORNEL CONTROL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 922)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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AGENCOURT 8863711 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6423902
5°, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                 LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu
                                                                                                                                      MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal
                                                                                                           ATGGAGGCTCATGCACTTACTATTAGGTTGACCAATAAAGTAGAATTTCCTTTTTTAGTT
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  CTTTTGATTTCTGGAGGTCACTGTCTGTTGGCATTAGTTCAAGGAGTTTCAGATTTTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="large_cell carcinoma"
/lab host="PHIOB (phage-resistant)"
/clome lib="NIH_MGC_18"
/clome lib="NIH_MGC_18"
/clome lib="NIH_MGC_18"
/note="Torgan: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT prinning. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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87.34%
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829596 MARC:
CF362328
CF362328.1
                                                                                                                           Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified cross_match v0.990329.

Plate: SRG8015 row: H column: 12
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                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2003)
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Smith, T. P.L., Freking, B.A., Ford, J.J., Vallet, J.L.,
Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.
A second set of porcine ESTs from a pooled-tissue no
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                                                                                                                                                                                                                                       Tel: 402 762 4366

Fax: 402 762 4390

Bmail: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                           Contact: Smith
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                     library
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                                                                                                           primer: TAGAAGGCACAGTCGAGG.
/organism="Sus scrofa"
/mol_type="mRNA"
                                                                                  Location/Qualifiers
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3PIG Sus scrofa cDNA 3',
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0166, USA
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', mRNA sequence.
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Buteleostomi; Sus.

with

EST

25-AUG-2003

862

805

685

160 626

745 180

Query DB:

Score:

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US-10-649-273-2_COPY_148_414 (1-267)
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   EST.
Gallus gallus (chicken)
Gailus gallus (chicken)
Gailus gallus
Eukaryota; Metazoa; Chordata; C
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                           sequence.
CF257246
CF257246.1
                                                                                                                  pha008_g02 PHA-activated
  Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuLeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArg
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                                                                                                                                                                                                                                                                                    PheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGly 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgLeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGlu
                                                                                                                                                                                  ACTCTGTTGTGTCCTCCCAGACTATGCACTGATAATGGCATTATGATTGCATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="MARC 3PIG"
/note="Vector: pcDNA3.1, Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including brain, liver, muscle, placenta/endometrium,
ovary, testes, and bone marrow."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="pooled"
/lab_host="DH108"
/clone_lib="MARC 3PIG"
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s gallus
              Phasianidae;
                           Euteleostomi;
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Wittzell,H., Bed'Hom,B., Morin,V., Yo
Chausse,A.M. and Zoorob,R.
A collection of chicken ESTs from act
Unpublished (2003)
Contact: Zoorob R
UPR 1983
                           575
  201
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Tel: 33 1 49 58 35 00
Fax: 33 1 49 58 33 81
Email: zoorob@vjf.cnrs.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNRS
                                                                                                                                                                                                                                                                                                                                                                                        LeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGly
                           GCAAGTAATCAGTATATCAGAAAAGGACTGCAGACTCTGGCAAATGCAAAACGGTTTTGCT
                                      AlaSorAsmRhoTyrileArgAlaLeuGlüileLeuThrAsmAlaThrGinCysThr
                                                                             TGCATGAAAAACAGCATATTATTACCAAAAACTGCAACTCTGGTTGTATCAGGAGGAGGAGTT
                                                                                       CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal
                                                                                                                              GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla
                                                                                                                                                                                                                                  CTTTTACTCTCCGGAGGTCACTGCATCTTGGCAGTAGCACGAGGAGTTTCAGATTTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu
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                                                                                                                                                                                 GAAAAAGAAGAAGGTATTCAAGAAGGGGAAATCCTGTCCTGCGTTAAGGACATCGCTGCT
                                                                                                                                                                                                                                                                                      CTGGCTCAAACCGGAGACTGGCAACAGTACACTTTCAGACTTCCCATGCAACAGTATCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Splenocytes"
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/note="Vector: pTriplEX2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Gallus
/mol_type="mRNA"
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                  Similarity:
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CK941819
CK941819.1
EST.
Bos taurus
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Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
Production of BST from cDNA libraries derived from immunologically activated bovine gut
                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: tads@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt "-trim fasta. Vector identified
by cross match using options -minmatch 12 -minscore 18
plate: 12 row: F column: 24
Seq primer: AGCGGATTACAATTTCACACAGG
                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 637.
Location/Qualifiers
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Animal and Natural Resources Institute
Bdlg. 200 Rm2A BARC-East, Beltsville, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CK941819 637 |
4065407 BARC 10BOV Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 3015048414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2004)
Contact: Tad S. Sonstegard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovinae; Bos.
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                                                                                                                       /dev stage="Mailtiple"
//lab_host="DBH10B T1 phage resistant"
/clone_lib="BARC 10BOV"
/clone_stage="Mailtiple"
/note="Organ: Small Intestine; Vector: pAgen-1; Site_1:
/note="Organ: Small Intestine; Vector: pAgen-1; Site_1:
ECORV; Site_2: Not1; Equimolar amounts of mRNA extracted
from proximal jejunums of 18 and 21 wk old steers, and
distal ileums of 14 day old calves. proximal jejunum
exposed to C. oncophora for 3 and 6 weeks, and distal
ileum exposed to C. parvum for 7 days"
                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9913"
/clone="10BOV12_F24"
                                                                                                                                                                                                                                                                               tissue_type="Pooled"
                                                                                                                                                                                                                                                                                                  'sex="Male"
                                                                                                                                                                                                                                                                                                                                               strain="Holstein"
                                                                                                                                                                                                                                                                                                                                                                              organism="Bos taurus"
   5.09e-87
838.00
92.47%
82.26%
60.51%
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Conservative:
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Email: est@watson.wustl.edu
Library constructed and donated by
Foundation for Biomedical Research,
                                                                                                                                                                               McCarrey, J., Eddy, M., Marra, M., Hillier, L. Martin, J., Wylie, T., Dante, M., Bowers, Y., Ritter, B., Tsagareishvili, R., Ronko, I., M. Bennett, J., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                               Mus
                                                                                 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                 Contact: McCarrey/Eddy NIEHS Mouse
                                                                                                                                                  Unpublished (2002)
                                                                                                                                                                  NIEHS Mouse
                                                                                                                                                                                                                                                                                                Mus musculus
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                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                  NIEHS Mouse
                                                                                                                                                                                                                                                                Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                              musculus (house mouse)
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Pante,M., Bowers,Y., Theising,B.,
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                                                                                                                                                                                                                                                                Craniata; Vertebrata; Sciurognathi; Muridae;
   by J. McCarrey, Ph.D.
rch, Dept. of Genetics)
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                                                                                  Louis,
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; Murinae; Mus
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                  (Southwest
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241 213 221 273 201 333

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Best Local Similarity:
Query Match:
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/dev_stage="60 day"
/lab_host="DH10B (phage-resistant)"
/clone_lib="McCarrey_Eddy spermatocytes"
/clone_lib="McCarrey_Eddy spermatocytes"
/note="Organ: testis; Vector: pBluescript_SK+
(Stratagene); Site 1: XhoI; Site 2: EcoRI; cDNA oligo
dT-primed [5'-(GA)10-ACTAGTTCGGAGTTTTTTTTTTTTTTTTTTTT] and
directionally cloned using 5' linkers 5'-AATTCGGCAGAG-3'
and 5'-CTCGTGCGG-3'. Size selection of >400bp material
gives average insert size ranging from 1-2 kb. Library was
mass excised (from lambda-UniZAP-XR) and resulting
single-stranded phagemids were prepped and tranformed
into DH10B. Library contains 98% recombinants.
References: J. Androl. 20:635-639 and Gene 25:263-269.
Library constructed and donated by J. McCarrey, Ph.D.
(Southwest Foundation for Biomedical Research, Dept. of
Genetics); excision done by E.M. Eddy, Ph.D. (National
Institutes of Health, National Institute of Environmental
Health Sciences). Original lambda-based library is
available through ATCC, catalog #63422."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 792)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W.
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubb
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 01612008930
Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Biomolecular Sciences University of Manchester Institute
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                                                                                                                                                                                          /Clone_lib="CSEQCHN59"
/Clone_lib="CSEQCHN59"
/note="Organ: limbs; Vector: pBluescript II KS(+); Site_1:
/note="Torgan: limbs; Vector: pBluescript II KS(+); Site_1:
/note="Torgan: limbs; Vector: pBluescript II KS(+); Site_1:
/note="Torgan: limbs; Vector: primary was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
/pollowing this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996: 791, except that a significantly longer
reannealing hybridization was used."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
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lab_host="DH10B"
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  1.01e-84
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Burt,D.W., Bosch,E., and Hubbard,S.J.

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EST.
Ovis aries (sheep)
Ovis aries
Bukaryota; Metazoa; C
Mammalia; Eutheria; C
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1 (bases 1 to 730)
Cossner, A. and Hopkins, J.
Ovine spleen\brain cDNA library
Unpublished (2004)
Contact: J Hopkins
                                                                                                                                                             CN823245
Oa splbn 04N08 M13reverse Sheep oa splbn 04N08 M13reverse Sheep oaries cDNA clone Oa splbn 04N08
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                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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AV602901.1 EST.
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AV602901
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High quality sequence stop: Location/Qualifiers
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                                                                                                                                                                             GCAGTCCAGCACACCGTAGCCTGCCACGTTGCNAAAAGAACACATCGCGCTATTCTGTTC
                                                                                                                                                                                                 ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe
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                                                           545 bp
Bos taurus kidney fetus
                                                  sequence.
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/mol_type="mRNA"
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Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukus)
Tel: 81-248-25-5641
Fax: 81-248-25-5725
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Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
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Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determ
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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oProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLe
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/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A
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/dev_stage="fetus"
/lab_host="DH10B"
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                                                TCTTGGAGTAGATATCAAAAAGAAGTTGGAGAAGCTGCTATAAAAGTGCCAAGATTAAA
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Search completed: February 16, 2005, 21:04:47 Job time: 3184.37 secs

Copyright

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

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Result
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Maximum Match 100%
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es. ctivity; IEA.	Euteleostomi; Homo.  242603899; r.G., Schuler G.D., Schuler G.D., Hsieh F., Hsieh F., Prange C., D., Mullahy S.J., Gunaratne P.H. L.J., Hulyk S.W., bbs R.A., Sanchez A., iffard G.G., Butterfield Y.S., Schein J.B., full-length human	07w668 bordetella 07wi34 bordetella 07wi34 bordetella 09clji pasteurella 07vqq9 candidatus 07nug9 candidatus 07nug9 candidatus 07nug chrombacte 06lv10 photobacter 067h2 hyacinthus 06fyfi bartonella 065xp0 manheimia 0915v7 pseudomonas 060986 aquifex aco 943764 haemophilus 082xn2 nitrosomona 0917a5 haemophilus

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Submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ295148; CAC14666.1; -.

R MEROPS; M22.004; -.

R Genew; HGNC:33075; OSGEPL1.

R GO; GO:0008450; F:O-sialoglycoprotein endopeptidase activity; IEA.

R GO; GO:0008233; F:peptidase activity; IEA.

R GO; GO:0008233; F:peptidase activity; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0008270; F:zinc io
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SEQUENCE
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2004 (TrEMBLrel. 26,
Putative sialoglycoprotease
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PIRSF: PIRSF004537; Osialglc_pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
ProDom; PD002367; Peptidase_M22; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RC STRAIN=CZECH II; TIJSUUE-Mammary tumor;

RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschal S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Holkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Sthein J.E.,

RA Krzywinski M.I., Skalska U., Smailus D.B., Schmerch A., Schein J.E.,

RA Krzywinski M.I., Skalska U., Smailus D.B., Schmerch A., Schein J.E.,

RA Krzywinski M.I., Skalska U., Smailus D.B., Schmerch A., Schein J.E.,

RA Krzywinski M.I., Skalska U., Smailus D.B., Schmerch A., Schein J.E.,
Query Match
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                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC058172; AAH58172.1; -
GO; GO:0008450; F:O-sialoglycoprotein endopeptidase acti
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase_M22.
InterPro; IPR009180; Peptidase_M22.
InterPro; IPR009180; Peptidase_M22.
InterPro; IPR009180; Peptidase_M21; IEA.
PIRSF; PIRSF004537; OSialglc_pptds; 1.
                                                                                                                                 PRINTS; PR00789; OSIALOPTASE. ProDom; PD002367; Peptidase M22; TIGRFAMs; TIGR00329; gcp; 1. Hypothetical protein. SEQUENCE 414 AA; 44962 MW; 04
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Q6PEB4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Generation and initial analysis of more than 15,000 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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hes 233; Conser
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88.9%; Score 1231; DB
87.3%; Pred. No. 4.6e-9
tive 15; Mismatches
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Statistic K., Itch H., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Statistic K., Itch M., Itch M., Itch M., Itch M., Itch M., Itch M., Ishin Y., Nakamura S., Hazama M., Nishine T., Harada A., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUB=Corpora quadrigemina;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-Corpora quadrigemina;

STRAIN-C57BL/6J; TISSUE-Corpora quadrigemina;

MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs

prepare full-length cDNA libraries for rapid discovery of new

Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
enriched library, clone:B230219017 product:similar to PUTATIVE
SIALOGLYCOPROTEASE TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Corpora The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature [3]
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01-MAR-2003
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
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Rodentia;
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criptome based on
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Sciurognathi; Muridae;
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on functional
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Murinae; Mus
                                                                                                            Carninci P.,
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RESULT Q9DONO ID Q9DONO OPPORT

Q9D0NO;

PRELIMINARY;

PRT;

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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Lost sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 10 days embryo whole body cDNA, RIKEN
enriched library, clone:2610001M19 product:similar
SIALOGLYCOPROTEASE TYPE 2.

full-length to PUTATIVE

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2 STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
2 Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
3 Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
4 Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
5 Akimura T., Hara A., Hashizume W.,
5 Akimura K., Ishii Y., Taroh M., Kagawa I., Kasukawa T.,
5 Akimira C., Matsuyama T., Miyazaki A., Konon H., Kouda M., Koya S.,
6 Akimirara C., Matsuyama T., Miyazaki A., Ohno M., Nakamura M.,
7 Akimirara K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
8 Aito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
8 Asasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
7 Agawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
7 An Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
8 Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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Best Local S
Matches 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G; GO:000845; F:O-sialoglycoprotein endopeptidase activity; GO; GO:000823; F:peptidase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0008270; F:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR001910; Peptidase M22.
Ffam; PF000814; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialglc_pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
PRODOm; PD002367; Peptidase M22; 1.
TIGRPAMS; TIGR00329; gcp; 1.
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388
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                     PKCPLGVDISKEVGEASIKVPQLKMEI 267
                                                                                                           ASNLYIRKALBIVANATOCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGVLHDVEDIRYE
                                                                                                                                               ASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYE
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14; Mismatches
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STRAIN=C57BL/G; TISSUE=whole body;

MEDINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K. Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K. Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=whole body;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
MEROPS; M22.004; ---
MGD; MGI:1919335; Osgepl1.
GO; GO:0008450; F:O-sialoglycoprotein er
GO; GO:0008233; F:peptidase activity; IE
GO; GO:0008270; F:zinc ion binding; IEA,
GO; GO:0008270; P:zinc ion binding; DEA,
GO; GO:0006508; P:proteolysis and peptid
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STRAIN-C57BL/6J; TISSUE=Whole body;
STRAINE-204993/74; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE-204993/74; PubMed=11042159; DOI=10.1101/gr.145100;
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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               peptidolysis;
                                                                                             IEA.
                                                                                                                             endopeptidase activity;
                   ΙEA
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                                                                                                                 RX PubMed=1247793; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RX Altschall S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RX Altschanko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RX Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
RX Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RX Villalon B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RX Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RX Alakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RX Alakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RX Alakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RX Alakesley R.W., Touchman J.W., Green E.D., Schnerch A., Schein J.E.,
RX Alones S.J. Marra M.A.;
RX Alones S.J. Marra M.A.;
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Best Local S
Matches 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00814; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialglc_pptds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6AYN7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR009180; Pept_M22_Osialg1.
Pfam; PF00814; Peptidase_M22; 1.
                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein (Fragment).
                                                                                                        Jones S.J., Marra M.A.;
                                                                                        Generation and initial analysis
                                                                         mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                N.A.
                                                       sequences.";
ad. Sci. U.S.A.
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29; gcp; 1.
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28, Last sequence update)
28, Last annotation updat
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Pred. No. 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                        99:16899-16903
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Scheetz T.E.,
                                                                                                                                                                                                                               Mullahy S.J., ratne P.H., Hulyk S.W.,
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Best Local S
Matches 214
The Subservall,

The PubMedel 14702039; DOI=10.1038/ng1285;

A Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

A Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

A Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

A Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

A Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

A Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

A Murakami K., Yasuda T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

A Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,

A Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,

A Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

A Tanani H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,

Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,

RA Togiya S., Komai P., Hara R., Takeuchi K., Arita M., Imose N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BC078974; AAH78974.1;
GG; GO:0008450; F:O-sialoglycoprotein endopeptidase act
GG; GO:0008270; F:Zinc ion binding; IEA.
GG; GO:000828; P:proteclysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase_M22;
InterPro; IPR00180; Pept M22 Osialgl.
R InterPro; IPR002016; Peroxidase.
Pfam; PF00814; Peptidase_M22; 1.
R PIRSF; PIRSF004337; Osialglc_pptds; 1.
R PIRSF; PR00788; OSIALOPTASE_
R PICKPAM8; TIGR00329; gcp; 1.
R PICKPAM8; TIGR00329; gcp; 1.
R PICKPAM8; TIGR00329; gcp; 1.
                                                                                                                                                                                                                                                                                                                                                                              Q96NH5 PRELIMINARY; PRT; 364 AA.
Q96NH5; PRT; 364 AA.
Q96NH5
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Butheria;
                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein FLJ30879. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Director MGC Project;
Submitted (AUG-2004)
                                                                                                                                                                                                                                                 TISSUE=Brain;
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. NON_TER 467 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50799
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Pred. No. 3.8e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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QBJFW3
ID QBJFW3
ID QBJFW3
ID QBJF
AC QBJF
O1-O
DT 01-O
DT 01-M
Brac
OC Buka
OC Acti
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CY
RN [1]
RP SEQU
RA Babb
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R MEROPS; M22.004; -.

R GO; GO:0008450; F:O-sialoglycoprotein endopeptidase activity; IEA.

R GO; GO:0008233; F:peptidase activity; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

DR GO; GO:0008508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR000905; Peptidase M22.

DR InterPro; IPR000905; Peptidase M22.

DR Pfam; PF000144; Peptidase M22; 1.

DR PINSF; PIRSF004537; Ostalglc pptds; 1.

DR PINSF; PR00789; OSIALOPTASE.

DR PRINTS; PR00789; OSIALOPTASE.

DR PRODOM; PD002367; Peptidase M22; 1.

DR TIGRFAMS; TIGR00329; gcp; 1.
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RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Hishigaki H., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Pujiwara T.,

RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,

RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,

RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Kawabata R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,

RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,

RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;

RT "Complas":

CDNAs":

CDNAs":

RT "Complete sequencing and characterization of 21,243 full-length human

RT CDNAs.":
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Best Local
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                                                                                                                                                                   Q8JFW3;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
SI:dZ211013.4 (Novel glycoprotease).
Name=dZ72B14.6;
                                                                                                         Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
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 Babbage A.;
Submitted (
                                      SEQUENCE PROM N.A.
                                                                                           Cyprinidae;
                                                                                                                                                                                                                                                                                  Q8JFW3
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EMBL; AK055441; BAB70923.1; -.
                                                                           TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 79.8%; Score 1105; DB 2; Similarity 98.6%; Pred. No. 2.5e-86; 14; Conservative 0; Mismatches 3
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                                                                                             Danio.
                                                                                                                                                                                                                                                                                    PRELIMINARY;
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 the EMBL/GenBank/DDBJ databases
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REROPS; M22.004;

GO; GO:0008450; F:O-sialoglycoprotein endopeptidase act
GO; GO:000823; F:peptidase activity; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0008270; F:peptidase M22;

InterPro; IPR000905; Peptidase M22;

R Pfam; PF00814; Peptidase M22;

R Pfam; PF00814; Peptidase M22;

R PIRSF; PROFF004537; Osialglc pptds; 1.

R PRINTS; PROFF00457; Osialglc ptds;

R PRINTS; PROFF00457; Osialglc ptds;

R PTIGRFAMs; TIGR00329; gcp; 1.
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Best Local Similarity
Matches 165; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=SI:d272B14.6;
Name=SI:d272B14.6;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Cypriniformes;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
SI:dC72B14.6 (Novel glycoprotease).
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InterPro; IPR009180; Pept M22 Osialgl.
Pfam; PP00814; Peptidase_M22; 1.
PIRSF; PIRSF004537; Osialglc_pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
PRODOm; PD002367; Peptidase_M22; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Clark G.;
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                                                                                                                                                                                                                                                                                                               activity;
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Li Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

C -i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

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Name=agCG46164; ORFNames=ENSANGG00000007922;

Anopheles gambiae str. PEST.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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ProDom; PD002367; Peptidase_M22; 1.
TIGRPAMS; TIGR00329; gcp; 1.
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                                                                                                                                         MQAHALMARMISTIPYPFLCLLVSGGHSLLVFVESTARFRLLGETLDDAPGEALDKIARR
                                                                                                                                                                      PKCPLGVDISKEVGEASIKVPQLKM
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                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                           32.7%; Score 453.5; DB 2; Length 401; 38.4%; Pred. No. 1.9e-30;
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01-DEC-2001
01-DEC-2001
01-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George Gonzalez M., Guarrin H., Li P., Liao G., Miranda A., Mungall C., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wa Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY051882; AAK93306.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda;
Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Berkeley;
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                                                                                                                                                                                                                                                                                                                            Similarity
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ASTRYDYD---SIDIOGSAGFA
                                                                         ASGGVASNFYIRRALBILTNATQCTLLCPPPRLCTDNGIMIAWNGIBRLRAGLGILHDIB
                                                                                                                          RARERAERTPPDGVISNYGDFCAGLLRSVSRHLMHRTQRAIEYCLLPHRQLFGDTPPTLV
                                                                                                                                                       MKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFC--KQRDLLPQNNAVLV
                                                                                                                                                                                                                 RRLSLIKHPECSTMSGGKAIEHLAK-QGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKII 117
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                              -GIRYEPKCPLGVDISKEVGEA
                                                           MSGGVANNDATYANIEHLAAQYGCRSFRPSKRYCSDNGVMIAWHGVEQL--
                                                                                                                                                                                     RRLRLHILPEYRLWNGGRAIEHAAQLASDPLAYEFPLPLAQQRNCNFSFAGIKNNSFRAI
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Last annotation update)
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AC Q9VWI
AC Q9VI
AC Q9VII
AC QOVII
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA Mannatides P.G., Scherer S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Goldek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kreinison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kreinison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kreinison J.A., Nelson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshreti A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Melbern D.R., Nelson D.L.,
RA Melson D.R., Nelson K.A., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Singson M., Skrong R., Shn B.,
RA Syler B.C., Siden-Kiamos I., Singson M., Skrong R., Shn B.,
RA Syler B.C., Schan M., Shang G., Zhao Q., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Ye J.,
RA Sheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Sheng X.H., Shang G., Zhong K., Shith H.O.,
RA Sheng X.H., Shith H.O.,
RA Sheng X.H., Shith H.O.,
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01-MAY-2000 (TrEMBLrel. 1:
01-MAX-2004 (TrEMBLrel. 26
CG14231-PA.
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Adams M.D., Celnik
Amanatides P.G., S
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01-MAY-2000
01-MAY-2000
                                                                                                                                                            MEDLINE-22426065; PubMed=12537568;
MEDLINE-22426065; PubMed=12537568;
Celniker S. B., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J.,
Svirskas R., Tabor P.B., Wan K., Stapleton M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.B., Myers B.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., C:
Patel S., Frise B., Wheeler D.A., Lewis S.E.,
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NCBI_TaxID=7227;
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   Carlson J.,
Rubin G.M.
                                       Svirskas
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Best Local Sim.
Matches 100;
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GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR009180; Peptidase M22.
Pfam; PP00814; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialglc pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
PRO0789; OSIALOPTASE.
PRO0789; D0002367; Peptidase M22; 1.
               O22145; Q8VWL2;
01-JAN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The transposable elements of the Drosophila me
a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
                                                                              022145
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FlyBase; FBgn0031060; CG14231.
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 O-sialoglycoprotein
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                                                                                                                                                                                                                                         ASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM
                                                                                                                                                        ASTRYDYD---SIDIQGSAGFA
                                                                                                                                                                                                                  MSGGVANNDAIYANIEHLAAQYGCRSFRPSKRYCSDNGVMIAWHGVEQL
                                                                                                                                                                                                                                                                                                                                      RRLRLHILPEYRLWNGGRAIEHAAQLASDPLAYEFPLPLAQQRNCNFSFAGIKNNSFRAI
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                                                                            PRELIMINARY;
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45328 MW; 9797F66E7D155538 CRC64;
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 endopeptidase (Sialoglycoprotease
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SEQUENCE
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC002387; AAB82636.2; -.
EMBL; AY024338; AAK00530.1; -.
EMBL; AY063864; AAL36220.1; -.
EMBL; AY117283; AAM51358.1; -.
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Submitted
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Town C.D.
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GO; GO:0008450; F:O-sialoglycoprotein endopeptidase GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0008270; F:sinc ion binding; IEA.

GO; GO:0008270; F:proteolysis and peptidolysis; IEA.

InterPro; IPR000905; Peptidase M22.

InterPro; IPR000905; Peptidase M22.

InterPro; IPR00180; Pept M22 Osialgl.

PIRSF; PRO0814; Peptidase M22; I.

PIRSF; PRO081637; Osialglc pptds; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L Carminci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker
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Arabidopsis thaliana (Mouse-east cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core er
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00789; OSIALOPTASE
ProDom; PD002367; Peptidase_N
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                                                                                                                                                                                                                                                                                                                                                       TIGRFAMs;
255
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                                                                                                                                                                                                                               Similarity
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1 K., Adamska I.;
WLGLDMH-----RSGGPAVEELALEGDAKSVKFNVPMKYHKDCNFSYAGLKTQVRLAIEA
                                                                                                                              MEAHALTIRLT-NKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVAR
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                                            RLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK
                                                                                                   MEAHALVARLVEQELS PPFMALLISGGHNLLVLAHKLGQYTQLGTTVDDAIGEAFDKTAK
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                                                                                                                                                                                                                                                                                                      480 AA;
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                  Peptidase_M22; 1.
29; gcp; 1.
                                                                                                                                                                                                                                                                                                      52995 MW;
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                                                                                                                                                                                                                         Score 407.5; DB 2
Pred. No. 2.1e-26;
                                                                                                                                                                                                                                                                                                      20DD6A86ACC1FFAD CRC64;
                                                                                                                                                                                                       Mismatches
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Matches 84
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Brownlie J.C., McGraw E.A., Martin W., Esser C., Ahmadinejad N.,
Wiegand C., Madupu R., Beanan M.J., Brinkac L.M., Daugherty S.C.,
Durkin A.S., Kolonay J.F., Nelson W.C., Mchamoud Y., Lee P.,
Berry K.J., Young M.B., Utterback T.R., Weldman J.F., Nierman W.C.,
Paulsen I.T., Nelson K.E., Tettelin H., O'Neill S.L., Eisen J.A.,
"Phylogenomics of the reproductive parasite Wolbachia pipientis wMel:
a streamlined genome overrun by mobile genetic elements.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0008450; F:O-sialoglycoprotein endopeptidase GO; GO:0008270; F:zinc ion binding; IEA. GO:0008270; F:zinc ion binding; IEA. GO:0006508; P:proteolysis and peptidolysis; IEA. InterPro; IPR000905; Peptidase M22. InterPro; IPR009180; Pept M22 Osialgl. Pfam; PF00814; Peptidase M22; 1. PIRSF; PIRSF004537; Osialglc_pptds; 1. PRINTS; PR00789; OSIALOPTASE. PRODOM; PD002367; Peptidase M22; 1.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMs; TIGR00329; gcp; 1.
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EMBL; AE017258; AAS14395.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wolbachia pipientis wMel.
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                                                                                                                                                                                                                                                                                                                       1 MEAHALTIRLTNKVEFPFLVLLISGGHCLLALVQGVSDFLLIGKSLDIAPGDMLDKVARR
                                                                                                                                                                                                                                                                                                                                                                         84;
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                                                                                                                                                                                 IGL-----SYPGGPLIEKLAKKGNGTRFKLFRAMIKRSGCNFSFSGIKTAVKNLVQEL
                                                                                                                                                                                                                             LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKK 120
                                                                                                                                                                                                                                                                             AVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGIGIL 231
                                                                                                                                      EKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGV
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  AANNFLREKLKOHIN---LNIFFPPNDLCTDNAIMVGWTGIERLQKNY--
                                          ASNETITRALETITIVATOCTLLCPPPRICTONGIMIAWNGIERLRAGIGILHDIEGIRYE 240
                                                                                            KMSB-----QDVCDVCASFQECISDILLDRVSNAIIMAESLNIKIND---FVITGGV
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                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              36634 MW;
                                                                                                                                                                                                                                                                                                                                                                                            26.6%;
                                                                                                                                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                                                                                                                                               Score 369; DB 2;
Pred. No. 2.8e-23;
6; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                F4914CDA58BC9390 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).
EMBL; AL591792; CAC47657.1;
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0008450; F:O-sialoglycoprotein endopeptidase
GO; GO:0008270; F:Z-sinc ion binding; IEA.
GO; GO:0006508; P:proteolygis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR009095; Peptidase M22.
InterPro; IPR0090180; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialgl. pptds; 1.
PIRSF; PIRSF004537; Osialgl. pptds; 1.
PIRSF; PIRSF004537; Osialgl. pptds; 1.
PIRSF, PIRSF004537; Peptidase M22; 1.
PIRSF, PIRSF004537; Peptidase M22; 1.
PIRSF PR007389; OSIALOPTASE.
PRODOM; PD002367; Peptidase M22; 1.
TIGRPAMS; TIGR00329; 9cp; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PROBABLE O-SIALOGLYCOPROTEIN ENDOPEPTIDASE (EC 3.4.24.57).
DRIVAGES-SMC03230;
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Complete proteome; Hydrolase.
SEQUENCE 360 AA; 37906 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=1021;
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## SUMMARIES

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Abu37844	Abu25741	Aay52203	Aar26325	Abg96491	Abo62704	Abu28771	Aau34711	Aay52204	Abu40069	Abu27480	Aab96423	Abu50237	Adf06228	Abu40514	Abu47561	Aau38187	Abb61112	Abu30280
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## ALIGNMENTS

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neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; immune disorder; rheumatoid arthritis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human metalloprotease MP1 fragment #1.
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WO200272751-A2

19-SEP-2002.

05-FEB-2002; 2002WO-US003353.

05-FEB-2001; 10-APR-2001; 2001US-0266518P. 2001US-0282814P.

(BRIM ) BRISTOL-MYERS SQUIBB CO.

Chen J, Feder J, Nelson TC, Duclos 'n Krystek

S

N-PSDB; 2002-723329/78. ABS76639.

New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and neurological disorders.

Claim 5; Page 29; 473pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding metalloprotease (MP-1). (I) is useful for preventing, treating, or

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Matches 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; immune disorder setumatoid arthritis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonis emphysema; cystic fibrosis; vascular disorder; inflammatory disorder; neurological disorder.
                                                                                                                                05-FEB-2001; 2001US-0266518P.
10-APR-2001; 2001US-0282814P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                   (BRIM ) BRISTOL-MYERS SQUIBB CO
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Pred. No. 7.9e-131;
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                                                24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or sepsis), pulmonary diseases (e.g. pneumonia, emphysema or cystic fibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This is the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and
                19-APR-2000; 2000CN-00106834
                                                                                  CN1318550-A.
                                                                                                                     Homo
                                                                                                                                                  Human; O-sialoglycoproteinase-like protein; OSGPLP; enzyme
                                                                                                                                                                                      Human O-sialoglycoproteinase-like protein SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1240; DB 5; ilarity 100.0%; Pred. No. 1.5e-130; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                        (first entry)
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Matches 239
                                                                                                                                                                                                                                                                     Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; anticonvulsant; cerebroprotective; antiparkinsonian; nootropic; antiinflammatory; antiulcer; hepatotropic; gynaecological; antibacterial; virucide; protozoacide; antiparasitic; cell proliferative disease; pMOD; protein modification and maintenance molecule; immunogenic fragment; cancer; autoimmune; inflammatory disease; neurological disorder; gastrointestinal; developmental; vesicle trafficking disorder; infection; gastrointestinal; developmental; vesicle trafficking disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents human O-sialoglycoproteinase-like protein (OSGPLP). The present invention also describes: (1) the preparation of the OSGPLP protein; (2) applying the OSGPLP protein in diagnosis; (3) the prevention and/or treatment of related diseases; (4) utilising the OSGPLP protein in screening its agonist, excitomotor and inhibitor and preparing an antibody against the OSGPLP protein; and (5) the use of the OSGPLP polynucleotide sequences, proteins, agonists, excitomotors, inhibitors and antibodies in treating diseases related to the abnormal OSGPLP gene and in preparing the medicine composite for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2003
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                                                                                                                                                                                                                                                     protein-protein interaction; drug-target interaction;
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Pred. No. 1.5e-130;
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06-JUL-2001; 2001US-0303445P.
13-JUL-2001; 2001US-0305405P.
09-AUG-2001; 2001US-0311442P.
24-AUG-2001; 2001US-0314921P.
29-AUG-2001; 2001US-0315992P.
03-MAY-2002; 2002US-0378205P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414 AA;
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Pred. No. 1.5e-130;
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                    New 38650, 28472, 5495 useful for diagnosing hematopoietic, brain,
                                                                                                                                                             08-NOV-2000; 2000US-0246768P.
08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
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            pharmacogenomics.
                                                                                       2002-759898/82
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                                                                                                             Kapeller-Libermann
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netalloprotease zinc glycoprotease sialoglycoprotease
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Best Local S
Matches 232
                                                                                                                                                                                                                                                                                                                              Cancer; aberrant cell proliferation; aberrant cell differentiation; breast cancer; ovarian cancer; prostate cancer; colon cancer; lung cancer; immune disorder; heart disorder; cardiovascular disorder; endothelial disorder; hematopoletic disorder; blood vessel disorder; brain disorder; pain; metabolic disorder; liver disorder; diabetes; platelet disorder; carcinoma; sarcoma; leukaemia; hedgkin's disease; autoimmune disorder; hypertension; atherosclerosis; heart failure; myocardial infarction; ischaemic heart disease; Crohn's disease; Grave's disease; Kawasaki syndrome; Raynaud's disease; aneurysm; cerebral ischaemia; peripheral neuropathy; Alzheimer's disease; enterpression of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
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97.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414
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Pred. No. 2.3e-126;
                                                                                                                                                                                                                                                                                                        nervosa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorder;
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Domain

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Glycoprotease\_domain

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes isolated 38650, 28472, 5495, 65507, 81588 and CC 14354 nucleic acid molecules (I) and their encoded polypeptides (II). The CS 38550 nucleic acid molecule comprises a sequence encoding adenosine CC deaminase. The 28472 nucleic acid molecule comprises a sequence encoding comprises a sequence encoding adenosine CC sequences that encode a human seven transmembrane domain (7TM). The CS 38550, 28472, 5495, 65507, 81588 and 14354 comprise CC sequences are useful for diagnosing, preventing or treating a subject CC with or at risk of developing a disorder, e.g. cancer or aberrant CC cellular proliferation and/or differentiation (e.g. breast, ovarian, CC prostate, colon or lung cancer), immune disorders, heart disorders, cardiovascular disorders, endothelial disorders, heart disorders, brain disorders, pain and metabolic disorders, CC liver disorders or platelet disorders. These disorders include carcinoma, CC sarcoma, leukaemia, Hodgkin's disease, autoimmune disorders, for ischaemic heart disease, Crohn's disease, Grave's disease, Kawasaki CC syndrome, Raynaud's disease, aneurysm, cerebral ischaemia, peripheral CC cachexia or diabetes. This is the amino acid sequence of the novel human CC cachexia or diabetes. This is the amino acid sequence of the novel human CC carbon or diabetes. This is the amino acid sequence of the novel human CC carbon or diabetes. This is the amino acid sequence of the novel human CC carbon or diabetes. This is the amino acid sequence of the novel human CC carbon or diabetes. This is the amino acid sequence of the novel human CC carbon or diabetes. This is the amino acid sequence of the novel human CC carbon or diabetes.
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Best Local S
Matches 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Fig 8A-B; 178pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-NOV-2000; 2000US-0246768P.
08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
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                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                            121
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356
                                     181
                                                                                                                                                                                            61 HFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC 120
                                                                                                                                                                                                                                                                                                                                             232;
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                                                                                                                                                                                                                                                                               1 LLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRF 60
                                                                                                          HLVKRTHRAILFCKQRDLLFQNNAVLVASGGVASNFYIRRALBILTNATQCTLLCPPPRL 180
                      CTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPOLKMEI 239
                                                                                                                                                                    HFDIKPPLHHAKNCDFSFTGLQHVTDKNNENRKQEEGIEKGQILSSAADIAATVQHTMAC
                                                                                                                                                                                                                                                           LLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRF
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                                                                                                                                                                                                                                                                                                                                               Conservative
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97.1%;
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Pred. No. 2.3e-126;
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65507,
disease
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ABU09569 ID ABU0

ABU09569

standard; protein;

414

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61

HPDIKPPLHHAKWCDFSFTGLQHYTDKIIMKKEKEEGIEKQQILSSAADIAATVQHTMAC

120

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                                                                                                                                   CC The invention relates to an isolated 38650 (encoding adenosine CC deaminase), 28472 (encoding a glycoprotease), 5495 (encoding a 7 cC transmembrane receptor), 65507, 81588 or 14354 nucleic acid molecule (or CC tasequence which is at least 60% identical to the six nucleic acids or CC their open reading frames, fragments of at least 15 nucleotides, CC naturally occurring variants, or a DNA insert of the plasmid deposited CC with the American Type Culture Collection as Accession No. not defined in CC the specification, which encodes the amino acid sequence). Also included CC are a host cell containing the nucleic acids (used to produce the CC the polypeptide, and identifying a compound that binds to/modulates the CC activity of the polypeptide. The nucleic acid molecules, polypeptides and CC methods are useful for diagnosing, treating cancer, aberrant cellular CC proliferation and/or differentiation, immune disorders, heart disorders, CC cardiovascular disorders including endothelial cell disorders, pain and metabolic disorders, liver disorders and platelet disorders (many CC examples of these disorders are given in the specification). The present
                                                                                Query Match
Best Local S
                                                                     Matches
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08-NOV-2000;
15-NOV-2000;
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immune disorders; heart disorder; brain disorder;
cardiovascular disorder; endothelial cell disorder; pain c
haematopoeitic disorder; blood vessel disorder; metabolic
liver disorder; platelet disorder; glycoprotease.
                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Fig 8; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated 38650, 28472, 5495, 65507, 81588 and 14354 nucleic acid molecules, useful for diagnosing, treating cancer, pain, or immune, heart, endothelial cell, hematopoeitic, blood vessel, brain, metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-2001;
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(KAPE/)
     37.5
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KAPELLER-LIBERMANN
GLUCKSMANN M A.
                                                                                    Similarity
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LLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRF
                                                                                                                                   414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders.
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                                                                                                                                                                 the Human glycoprotease encoded by cDNA
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2000US-0246772P.
2000US-0249185P.
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                                                                 Score 1203; DB 6;
Pred. No. 2.3e-126;
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                                                                                                Length 414;
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                                                                                                                                               Query Match
Best Local S
Matches 186
                                                                                                                                                                                                                         The present invention relates to novel human secretory or membrane proteins (ADA54712-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                        Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease.
                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                      Claim 14; SEQ ID NO 2039; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-395539/38.
N-PSDB; ADA52832.
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24-JAN-2002; 2002US-0350435P.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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                 121
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                                                                                                                                                186;
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                                                                                                                                                             Similarity
HLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRL
                                                                   HFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC
                                                                                           LALVQGVSDFLLLGKSLDIAPGDMLDKVARRLPLIKHPECSTMSGGKAIEHLAKQGNRF
                                                                                                             LLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALBILTNATQCTLLCPPPRL 180
                                                                                                                                                                                                  364 AA;
                                                                                                                                                 Conservative
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                                                                                                                                                           77.4%;
98.4%;
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Hio Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                             0; Mismatches
                                                                                                                                                           Score 960; DB 6
Pred. No. 5e-99;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventior useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL016175) and the enco-deligation (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 409 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes from Drosophila
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N-PSDB; ABL13236.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC,
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11-JUL-2000; 2000US-00614150
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pharmaceutical.
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                                                                                                                                                        HFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC
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HLMHRTQRAIEYCLLPHRQLFGDTPPTLVMSGGVANNDAIYANIEHLAAQYGCRSFRPSK 346
                                                   HLVKRTHRAILFC--KQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPP 178
                                                                                                          AYEFPLPLAQQRNCNFSFAGIKNNSFRAIRARERAERTPPDGVISNYGDFCAGLLRSVSR
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                                                                                                                                                                                                                                                                                                                                  Conservative
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a and
                                                                                                                                                                                                                                                                                                                                                            26.8%; Score 332.5; DB 4; 35.9%; Pred. No. 3.9e-28;
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                                                                                                                                                                                                                                                                                                                                  38;
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                                                                                           Query Match
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Matches 82
                                                                                                                                                                                               Proteins AAY52202-Y52217 encompass a novel family of proteins designated the ygjD family, after the name given to the Escherichia coli family member. These proteins are essential for the survival of both Gram negative and Gram positive bacteria, although no function has as yet been ascribed to these proteins. The ygjD proteins, fragments of ygjD proteins (for example, fragments encompassing one or more conserved ygjD motifs such as AAY52218-Y52284) and nucleotides encoding them can be used to identify antagonists and broad spectrum antibacterial compounds. These antagonists and compounds can be used to treat a wide range of bacterial infections. New antibiotics are urgently needed, as serious bacterial infections and antibiotic resistant strains are becoming increasingly prevalent. The proteins of the invention are essential proteins for bacterial viability, and represent new targets for antibiotics
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                                                                                                                                                                   Sequence 463 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel bacterial polypeptides used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Fig 1; 55pp; English.
                                                                                             82; Conservative
                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLAXO GROUP LTD
                  RLCTDNGIMIAWNGIERLRAGLGILHDIE-GIRYEPKCPLGVDISKEVGEA
                                             LLALVÇGVSDFILLGKSLDIAFGUMLÜKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "ygjD conserved
152. .198
/note= "ygjD conserved
208. .259
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                                                                                                            26.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loferer
                                                                                           34;
                                                                                          Score 326; DB 3; 1
Pred. No. 2.6e-27;
4; Mismatches 84;
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                                                                                                                           Length 463;
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29-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment
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hybridisation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .25.7%; Score 319; DB 3; Length 245; Iarity 36.2%; Pred. No. 6.2e-27; Conservative 31; Mismatches 82; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                 sequence.
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11-MAY-1999
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   Arabidopsis thaliana
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   AAG19285
   06-SEP-2000
   EP1033405-A2
   termination
   25-FEB-2000;
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   81;
   μ
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| 222222222222                                                                                                                                                         | 99US-0142154P<br>99US-01422390P<br>99US-0142390P<br>99US-0142803P<br>99US-0142970P<br>99US-0143542P<br>99US-0144065P<br>99US-0144065P<br>99US-0144085P<br>99US-014431P<br>99US-014431P<br>99US-0144331P<br>99US-0144332P<br>99US-0144334P<br>99US-0144334P | 99US-0139455P<br>99US-0139457P<br>99US-0139458P<br>99US-0139459P<br>99US-0139461P<br>99US-0139461P<br>99US-0139462P<br>99US-0139673P<br>99US-0139763P<br>99US-0139899P<br>99US-0140353P<br>99US-0140353P<br>99US-0140353P<br>99US-0140655P<br>99US-0140654P<br>99US-0140654P<br>99US-0140654P<br>99US-0140654P<br>99US-0140654P<br>99US-0140654P                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 99US-013421P. 99US-013427P. 99US-0134768P. 99US-0135124P. 99US-0135124P. 99US-0135124P. 99US-0136021P. 99US-0136021P. 99US-0137722P. 99US-0137722P. 99US-0137724P. 99US-0138044P. 99US-0138044P. 99US-0139119P.                                                                     |
|                                                                                                                                                                      |                                                                                                                                                                                                                                                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|                                                                                                                                                                      |                                                                                                                                                                                                                                                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :                                                                                                                                                                                                                                                                                                                                                                                                                                         |
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|                                                                                                                                                                      | א מ<br>א א א א א א א א א א א א א א א א א א                                                                                                                                                                                                                 | אק<br>אק אק                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| 14-OCT-199 14-OCT-199 14-OCT-199 18-OCT-199 21-OCT-199 21-OCT-199 21-OCT-199 21-OCT-199 21-OCT-199 21-OCT-199 21-OCT-199 21-OCT-199 22-OCT-199 22-OCT-199 22-OCT-199 | 20-SEP-199 22-SEP-199 23-SEP-199 24-SEP-199 24-SEP-199 29-SEP-199 06-OCT-199 06-OCT-199 06-OCT-199 11-OCT-199 113-OCT-199 113-OCT-199 113-OCT-199 114-OCT-199                                                                                              | 17-AUG-199 20-AUG-199 20-AUG-199 20-AUG-199 23-AUG-199 23-AUG-199 23-AUG-199 25-AUG-199 27-AUG-199 27-AUG-199 27-AUG-199 30-AUG-199 31-AUG-199                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 111111100066<br>1111111100066<br>1111111100066                                                                                                                                                                                                                                                                                                                                                                                            |
| 010 - 010<br>010 - 010                                       | 9US - 0.11<br>9US - 0.11                                                                         | 003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003-011<br>003 | 99US-0145276P<br>99US-0145913P<br>99US-0145918P<br>99US-0145951P<br>99US-0146388P<br>99US-0146388P<br>99US-0147303P<br>99US-0147204P<br>99US-0147204P<br>99US-0147303P<br>99US-0147303P<br>99US-0147303P<br>99US-01474368P<br>99US-01474368P<br>99US-0148341P<br>99US-0148341P<br>99US-0148341P<br>99US-0148341P<br>99US-0148341P<br>99US-01483684P                                                                                       |
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RESULT 14
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  25-OCT-1999;
25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
   21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
  Claim 25; SEQ ID NO 50858; 1766pp; English.
   N-PSDB; ACA26804.
  21-MAR-2002; 2002WO-US009107
   03-OCT-2002
  WO200277183-A2
  Bordetella pertussis
  Antisense; prokaryotic essential gene; cell proliferation; drug design
  Protein encoded by Prokaryotic essential gene #8461.
   19-JUN-2003
  ABU22934;
   ABU22934 standard; protein; 382
  (ELIT-)
  8-OCT-1999;
8-OCT-1999;
   -0CT-1999;
   2003-029926/02.
   173
   284 SVKFNVPMKYHKDCNFSYAGLKTQVRLAIBAKE----IDAKCPVSSATNEDRRNRADIAA
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99US-0161992P.
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  99US-0161360P.
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Carr G
  25.7%;
  INC.
   ည်
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Pred. No. 1.5e-26;
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   Haselbeck R, Yamamoto R,
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Forsyth
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  Zyskind JW;
Xu HH;
   30;
   Gaps
  339
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The invention relates to an isolated nucleic acid comprising any one

of

21-MAR-2002; 2002WO-US009107.

WO200277183-A2

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RESULT 15
ABU35232
   the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(C) if we vector comprising a promoter operably linked to the nucleic acid cenciding a polypeptide whose expression is inhibited by the antisense concleic acid; (4) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the cantisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a gene in an operon required for consideration, or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of the strains; or (13) identifying the target of a compound that inhibits the collular proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation in cells other than S. aureus, S. typhimurium, crequired for proliferation in cells other than S. aureus, S. typhimurium, crequired for proliferation of the printed specification, but was obtained in electronic format directly from WIPO at
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   Matches
  Query Match
   Sequence 382 AA;
  Moraxella catarrhalis
   Antisense; prokaryotic essential
  Protein encoded by Prokaryotic essential gene #20759
  19-JUN-2003
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  ABU35232 standard; protein; 348 AA
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   181
  287
  121 HLVKRTHRAILFCKORDLLPQNNAVLVASGGVASNFYIRRALEILTNATOCTLLCPPPRL 180
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  62 PDIKPPLHHAKNCDFSFTGLQ-HVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC 120
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  Length 382;
   Indels
   20;
   Gaps
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   the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid cencoding a polypeptide whose expression is inhibited by the antisense comprising the vector; (3) an isolated concleic acid; (4) a host cell containing the vector; (3) an isolated continuously peptide or its fragment whose expression is inhibited by the cartivity of an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway for the gene product or that has an activity against a biological pathway of a gene or its gene product or that has an activity against a proliferation of the biological pathway in which a proliferation, or that inhibits cellular proliferation of an compound that inhibits proliferation of an compound's activity; (11) a culture comprising strains in which the gene conduct is overexpressed or underexpressed; (12) determining the extent convolute activity and inhibits are useful for cellular proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational conduction of for cellular proliferation of conduction of a contract processed.
   Query Match
Best Local S
Matches 66
   Wang L,
Wall D,
  drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
   21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
   Sequence
   ftp.wipo.int/pub/published_pct_sequences
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  Claim 25; SEQ ID NO 63156; 1766pp; English.
  (ELIT-) ELITRA PHARM INC.
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   , Ohlsen
Forsyth
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   Zyskind JW;
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   Gaps
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306 CTDNGAMIAYAGFCRLSCG 324

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Search completed: February 16, 2005, 13:05:57 Job time: 49.0598 secs

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|--------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------|------------------------------------------------------------------|--------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 음 성 음                                                                                                                    | হ ৪ হ                                                                                              | 음 성                                                              |                                                              | US-<br>S G G G G G G G G G G G G G G G G G G G                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |            | 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|                                                                                                                          |                                                                                                    |                                                                  | Query Match<br>Best Local<br>Matches 23                      | RESULT 1 US-10-067-44 Sequence 2 Patent NO. GENERAL IN APPLICANT TITLE OF TITLE OF FILE REFE CURRENT A CURRENT A CURRENT A PRIOR APP PRIOR APP PRIOR APP PRIOR FIL NUMBER SEQ ID NO LENGTH ORGANISM US-10-067-44                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |            | 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| 149 HL<br>181 CT<br>209 CT                                                                                               | 61 HE<br>89 HE                                                                                     | 1 LL<br>  <br>29 LL                                              | atc<br>cal                                                   | RESULT 1  US-10-067-443-22  US-10-067-443-22  Sequence 22, Application US/10  Patent No. 6642041  GENERAL INFORMATION: APPLICANT: Bristol-Myers Squi ITILE OF INVENTION: POLYNUCLE ITILE OF INVENTION: SPINAL C FILE REFERENCE: D0073 NP CURRENT FILING DATE: 2002-02  PRIOR APPLICATION NUMBER: US PRIOR APPLICATION NUMBER: US PRIOR PILING DATE: 2001-02-05  PRIOR PILING DATE: 2001-04-10 NUMBER OF SEQ ID NOS: 71  SOFTWARE: PATENTIN OS: 71  SOFTWARE: PATENTIN OS: 71  SOFTWARE: PATENTIN OS: 71  SOFTWARE: PATENTIN OS: 71  TYPE: PRT  ORGANISM: homo sapiens  US-10-067-443-22                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |            | 173<br>148.5<br>117<br>94.5<br>94.5<br>89.5<br>89.5<br>81.5<br>79<br>79<br>79<br>79<br>79<br>79<br>78                                                                                                                                                                                                                                                                                                                                                                            |
| VKRTHRA: DNGIMIAI                 DNGIMIAI DNGIMIAI                                                                      | DI KPPLHI<br>       <br>DI KPPLHI<br>VKRTHRA:                                                      | ALVQGVSI<br>       <br>ALVQGVSI                                  | h 100<br>Similarity 100<br>39; Conservative                  | 3-22 2, Application US/10067443 6642041 FORMATION: SPISTON: SQUIDS COMINIVENTION: SPINAL CORD, POLYNUCLEOTIDE INVENTION: SPINAL CORD, POLYNUCLEOTIDE OF COMINICATION NUMBER: US/10/0 POLYNUCLEOTIDE OF COMINICATION NUMBER: US/10/0 POLYNUCLEOTIDE US/10/0 POLYNUCLEOTION OF COMINICATION NUMBER: US/0/266 LICATION NUMBER: US/0/266 LICATION NUMBER: US/0/266 LICATION NUMBER: US/0/266 LICATION NUMBER: US/0/267 LICATION NUMBER: US/0/267 LICATION UNDER: US/0/266 LICATION UNDER: US/0/266 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: US/0/282 LICATION UNDER: U                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |            | 124<br>9.4<br>7.6<br>6.7<br>7.6<br>6.3<br>6.3<br>6.3<br>6.3                                                                                                                                                                                                                                                                                                                                                                                                                      |
| ANGIERI                                                                                                                  | TLFCKQF                                                                                            | OFILLIGE<br>                                                     | 100.09<br>100.09<br>vative                                   | ion US/10067  Vers Squibb  POLYNUCLEOTI  SPINAL CODD  3 NP  NUMBER: US/1  2002-02-05  MBER: US 60/  901-02-05  MBER: US 60/  901-04-10  171  271  271  271  271  271  271  2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |            | 366<br>340<br>292<br>480<br>481<br>214<br>214<br>214<br>214<br>217<br>1072<br>1072<br>1072<br>1137<br>1137<br>1137<br>1137<br>334<br>334<br>334                                                                                                                                                                                                                                                                                                                                  |
| # <u></u> ###################################                                                                            | TICE SET                                                                                           | E — E                                                            | 9 9<br>3 ;                                                   | 3. 10<br>5.05<br>7.10<br>1. 10<br>1. |            | בק d d d d d d d d c α α α α α α α α α α α                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| HIVKRTHRAILFCKQRDILFQNNAVLVASGGVASNFYIRRALBILTNATQCTLLCPPPRL CTDNGIMIAMNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI | HFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC<br>                                   | LLALVOGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRF<br> | Score 1240; DB 4;<br>Pred. No. 5.6e-145;<br>0; Mismatches 0; | 3<br>ENCODING A<br>MP-1<br>5,518<br>5,518<br>2,814                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ALIGNMENTS | US-09-134-000C-4956. US-10-067-443-6 US-10-067-443-6 US-09-724-623-81 US-09-583-110-5050 US-09-138-352-4609 US-09-328-352-4609 US-09-902-540-13841 US-08-264-002-5 US-09-902-540-15572 US-08-083-945C-2 US-08-083-945C-7 US-09-252-991A-31318 US-09-252-991A-31318 US-09-538-092-968 US-08-536-929-968 US-08-536-924-94 US-08-536-240-2 US-08-888-429A-4 US-09-149-79-4 US-09-149-79-4 US-09-057-009-4                                                                           |
|                                                                                                                          | QILSSAADIAATVQHTMAC 120<br>                <br>QILSSAADIAATVQHTMAC 148<br>LEILTNATQCTLLCPPPRL 180~ | STMSGGKAIEHLAKQCNRF 60                                           | Length 267;<br>Indels 0; Gaps 0;                             | NOVEL METALOPROTEASE HIGHLY EXPRESSED                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |            | Sequence 4956, Appli<br>Sequence 81, Appli<br>Sequence 8150, Ap<br>Sequence 5050, Ap<br>Sequence 3197, Ap<br>Sequence 11841, A<br>Sequence 11841, A<br>Sequence 5, Appli<br>Sequence 7, Appli<br>Sequence 7, Appli<br>Sequence 7, Appli<br>Sequence 31318, A<br>Sequence 968, Appli<br>Sequence 4, Appli |
|                                                                                                                          |                                                                                                    |                                                                  |                                                              | ED                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            | * 3                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |

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; Sequence 2, Application US/10067443
; Patent No. 6642041
; GENERAL IMPORMATION:
; APPLICANT: Bristol-Myers Squibb Company

RESULT 2 US-10-067-443-2

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; LENGTH: 414
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CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 2
   8
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  ; TYPE: PRT
; ORGANISM: homo
US-10-067-443-19
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  US-10-067-443-19
  Sequence 19, Appl
Patent No. 664204
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Best Local Similarity
   SEQ ID NO 19
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   Query Match
Best Local Similarity
   FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
   APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
   TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED TITLE OF INVENTION: SPINAL CORD, MP-1
   NUMBER OF SEQ ID NOS: 71
SOPTWARE: PatentIn version 3.0
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  238;
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   61 HFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGI-----
   1 LLALVQGVSDFLLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRF
   1 LLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRF
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   CTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI 239
   HLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRL
  HFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC
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  Application US/10067443
   100.0%; Score 1240; DB 4; ilarity 100.0%; Pred. No. 1.1e-144; Conservative 0; Mismatches 0;
  Conservative
  sapiens
  sapiens
  2001-04-10
   97.9%;
  Score 1213.5; DB 4;
Pred. No. 2.3e-141;
0; Mismatches 1;
  Length 414;
  Indels
   Length
   439;
  25;
   0;
  Gaps
   Gaps
   235
   355
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  US-10-067-443-3
  Sequence 2726, Application US/09540236 Patent No. 6673910
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CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
NUMBER OF SEQ ID NOS: 3840
  ORGANISM: Arabidopsis thaliana
  TYPE: PRT
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   225
   383
  181
   326
   121
  276
   356
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   61
   99
  , Application US/10067443 6642041
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   VGEA 228
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  PLGVDISKEVGBASIKVPQLKMBI 239
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  PLGVDISKEVGEASIKVPQLKMBI
  Conservative
  439
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GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OP INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARI
TITLE OP INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
  APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED IN
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
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   CTDNGIMIAWNGIERLRAGLGILHDIEGIRYE-----PKCPLGVDISKE 224
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  --- EKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLFQNNAVLVASGGVASN 155
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  26.3%; Score 326; DB 4; 33.6%; Pred. No. 2.7e-31; tive 34; Mismatches 84
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   -----IRNRADIAASFQRVAVL
  Length 463;
  Indels
  44;
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  180
  355
   432
   382
   325
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                        US-09-543-681A-6513
   RESULT 7
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  US-09-252-991A-17372
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  ; TYPE: PRT ; ORGANISM: M.catarrhalis US-09-540-236-2726
  US-09-252-991A-17372
Sequence 6513, Application US/09543681A
  Query Match
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CURRENT FILING DATE: 1999-02-18
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PRIOR FILING DATE: 1998-07-10
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   APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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  ENGTH:
   Local Similarity
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   202
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   61 HFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC 120
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   1 LLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRF
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  Similarity
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   TLVKKCTKALQMTGIRQ-----LVVAGGVSANQTLRRTLTETLRQIDASVYYAPTEL 307
   TDNGAMIAYAGCORLLAG---QHDGPAISVQPRWPM 395
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   CIDNGAMIAYAGFCRLSRGQSDDLAVRCIPRWDMIMLGIBYD 349
  TDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPL 217
  Conservative
   Conservative
  18.6%; Score 231; DB 4; L
33.8%; Pred. No. 1.3e-19;
34. Mismatches 87;
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   Gaps
  255
   60
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US-08-087-797-3
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CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
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APPLICANT:
  LENGTH: 357
                 NAME: Layton, Jr., Samuel G.
REGISTRATION NIMEEE: 22207
REFERENCE/DOCKET NUMBER: 337.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 704 377 1561
   APPLICATION NUMBER: US/0
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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  212 FVFPRPMTDRPGLDFSFSGLKTFAANTIRQNDDSE-----QTRADIARAFEDAVVDT 263
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  Similarity
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   Application US/08087797
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  FDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACH 121
  GARY BRETON
   1211 East Morehead
   Mellors, Alan
Lo, Reggie Y.C.
Abdullah, Khalid M.
   PatentIn Release #1.0, Version #1.25
   United States
704 334 2014
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INFORMATION FOR SEQ ID NO:

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RESULT 10
_ US-10-067-443-4
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Matches
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CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
   APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
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; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-067-443-4
  US-10-067-443-28
  US-10-067-443-28
  GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED IN
TITLE OP INVENTION: SPINAL CORD, MP-1
TITLE OP INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT PAPLICATION NUMBER: US/10/067,443
CURRENT PILING DATE: 2002-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-05
   SOFTWARE: PatentIn version 3.0 SEQ ID NO 4
   SEQ ID NO 28
  Sequence 28, Application US/10067443 Patent No. 6642041
  Query Match
Best Local Similarity
  GENERAL INFORMATION:
  Best Local Similarity 27.
   Query Match
  Matches
   Patent No.
   Sequence 4, Application US/10067443
  APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: SPLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPLYAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER: OF SEQ ID NOS: 71
NUMBER: OF SEQ ID NOS: 71
   SOFTWARE:
   NUMBER OF SEQ ID NOS: 7
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TYPE: PRT
ORGANISM: Caenorhabditis elegans
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  EASIKVPQLKM 237
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  Length
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   US-08-087-797-2
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   Query Match
Best Local (
  Patent No.
  Sequence 2,
  Matches
  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
-08-087-797-2
   ATTOKNESS.

NAME: Layton, Jr., Samuel NAME: Layton, Jr., Samuel NAME: Layton, Jr., Samuel NAME: Layton, Jr., Samuel NAME: 22807

REGISTRATION NUMBER: 3374-

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 1.561
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,797
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
   GENERAL INFORMATION:
APPLICANT: Mellor
   TELEFAX: 704 334 2014
INFORMATION FOR SEQ ID NO: 2:
   APPLICANT: Lo, Reggie
APPLICANT: Abdullah,
TITLE OF INVENTION: F
  SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acid
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  ATTORNEY/AGENT INFORMATION:
NAME: Layton, Jr., Samuel G.
   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson, P.A.
   TITLE OF INVENTION:
  CITY: Charlotte
STATE: No. 5543312th Carolina
   Local
   COUNTRY:
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  Application US/08087797
   ---IDTPRRKL 392
   1211 East Morehead Street,
  325 amino acids
   United States
  Conservative
  Abdullah, Khalid M
   Lo, Reggie Y.C.
   Mellors, Alan
  16.1%; Score 200; DB 1; L
31.6%; Pred. No. 6.5e-16;
31.6%; Mismatches 91;
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   3374-80
   Version #1.25
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8277
INFORMATION FOR SEQ ID NO: 6609:
   PRIOR APPLICATION NUMBER: 60/085,598
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
   Local Similarity
   MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
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   CITY: Waltham
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  SOFTWARE:
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  DDRESSEE: GENOME THERAPEUTICS CORPORATION
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PRIOR FILLING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 327
TYPE: PRT
ORGANISM: Thermotoga maritima
US-10-067-443-5
  US-08-987-121A-4
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   Sequence 4, Application US/08987121A
GENERAL INFORMATION:
APPLICANT: Hoskins, Jo Ann
APPLICANT: Trang, Joseph Chiou-Chung
APPLICANT: Treadway, Patti Jean
TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence
TITLE OF INVENTION: GCP
   GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED

TITLE OF INVENTION: SPINAL CORD, MP-1
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15.6%; Score 193.5; DB 4
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CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
  FILE REFERENCE: D0073 NP
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
COMPUTER READABLE FORM:
  NUMBER OF SEQUENCES:
   STREET: Lilly Corpo
CITY: Indianapolis
STATE: Indiana
                     COUNTRY: U
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SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US/08/987,121A
PILING DATE:
CLASSIFICATION: 435
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
   ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKST NUMBER: X-
  TELECOMMUNICATION INFORMATION:
   TELEPHONE: 317-276-3334
TELEPHONE: GRO ID NO: 4:
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US-10-649-273-22

US-10-661-722-22

US-10-667-443-2

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| 350  | 421              | 421               | 421              | 421   | 421              | 421          | 396  | 337                  | 337                 | 441                  | 341                  | 335    | 337                  | 41               | 340                  | 337                  | 337                 | 342                  | 342                 | 347              | 341                  | 341                 | 251             | 343   | 312                  | 348                  | 333              | 382              | 444                  | 463               | 463               |
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| 5366 | 28,              | Sequence 4, Appli | 28,              | 4,    | 28,              | .4           | 671  | ው                    | $\mathbf{r}$        | Sequence 111620,     |                      |        | 781                  |                  |                      | Sequence 75485, A    |                     | Œ                    | 1104                |                  | Œ                    | 1179                |                 | 67227 |                      | 631                  | N                |                  | ro<br>               | Sequence 3, Appli | Sequence 3, Appli |

## ALIGNMENTS

US-10-067-443-22

GENERAL INFORMATION:

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Sequence 22, Application US/10067443 Publication No. US20030082782A1

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US-10-067-443-22
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   Query Match
Best Local Similarity
Matches 239; Conserva
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CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
  APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
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CURRENT FILING DATE: 2003-08-29
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PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
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PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2002-04-05
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TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
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SOFTWARE: PatentIn version 3.2
   APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
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   Gaps
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TITLE OF INVENTION: SPINAL CORD, MP-1
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FILE REFERENCE: DO073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF ESO ID NOS: 71
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RESULT 5
US-10-649-273-2
; Sequence 2, Application US/10649273
; Publication No. US20040043407A1

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CURRENT FILING DATE: 2003-08-27
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PRIOR FILING DATE: 2001-02-05
PRIOR PRIOR HELING DATE: 2001-02-05
PRIOR ETLING DATE: 2002-02-05
PRIOR ETLING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 2
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   ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-649-273-2
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  Sequence 2, Application US/10651722 Publication No. US20040048302A1 GENERAL INFORMATION:
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
   NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
  PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
   APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
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  CTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI 414
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ilarity 100.0%;
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Publication No. US20040043407A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REPERENCE: D0073 CNT
   PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.0
SEQ ID NO 19
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Publication No. US20030082782A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED IN

TITLE OF INVENTION: SPINAL CORD, MP-1

FILE REFERENCE: D0073 NP

CURRENT APPLICATION NUMBER: US/10/067,443

CURRENT PILING DATE: 2002-02-05

PRIOR PILING DATE: 2001-02-05

PRIOR PILING DATE: 2001-02-05

PRIOR PILING DATE: 2001-02-05
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CURRENT FILING DATE: 2003-08-27
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PRIOR APPLICATION NUMBER: US 10/067,443 PRIOR FILING DATE: 2002-02-05 PRIOR APPLICATION NUMBER: US 60/282,814

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; ORGANISM: homo sapiens
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CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
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  SOFTWARE: PatentIn version 3.2
  APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
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Sequence 2039, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO APPLICANT: SUGIYAMA, TO

APPLICANT:

APPLICANT:

SUGIYAMA, TOMOYASU OTSUKI, TETSUJI WAKAMATSU, AI SATO, HIROYUKI

ISHII, SHIZUKO

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PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR FILING DATE: 2000-11-15
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FILE REFERENCE: 381552004990
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APPLICANT: Kapeller-Libermann, l
APPLICANT: Glucksmann, Maria A.
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  APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
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TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
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TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED IN
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT ENLIGHTON NUMBER: US/10/667,443
CURRENT APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-04-10
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US-10-649-273-3

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CURRENT FILING DATE: 2003-08-27
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PRIOR FILING DATE: 2001-02-05
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PRIOR FILING DATE: 2002-02-05
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PRIOR PILING DATE: 2001-04-10
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|-----------|---------|----------|-----------|-----------|-------------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|----------|----------|----------|-----------|------------|-------------|----------|-----------|----------|----------|----------|-----------|----------|---------|-----------|----------|----------|----------|----------|----------|----------|----------|-------------|---------|-------|-----------|----------|
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| ٣         | •       | ــر د    | 8         | _         | N           | œ        | 8         | œ         | 8         | œ         | w         | w         | N         | Φ        | თ        | w        |           |            |             | ຫ        |           |          | 10       | N        | N         | 9        | 0       | ഗ         | u        | ທ        | 10       | 10       | 9        | 6        | 10       | 10          | σ       | თ     | 9         | 6        |
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## ALIGNMENTS

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| cores:<br>llarity:<br>Similarity:                                                           | Zhang,J., zh<br>Wang,J., and<br>Wucleic acid<br>Patent: US (<br>Loc<br>/ou<br>/mc                                                                                                                                                              | Unknown. Unknown. Unclassified. 1 (bases 1 to 1416) Tang, Y.T., Zhou, P.,                                                   | AR541929<br>Sequence 177 from paten<br>AR541929<br>AR541929.1 GI:53934009 |
| 2.242-113<br>1240.00<br>100.00%<br>100.00%<br>100.00%                                       | Zhang, J., Zhao, Q.A., Yang, Y., Xue, A.J<br>Wang, D. and Drmanac, R.T.<br>Nucleic acids and polypeptides<br>Patent: US 6743619-A 177 01-JUN-2004;<br>Location/Qualifiers<br>11416<br>/organism="unknown"<br>/mol_type="genomic DNA"           | l.<br>to 1416)<br>hou,P., Goodr                                                                                             | ir                                                                        |
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|                                                                                             | Wang, JR.,                                                                                                                                                                                                                                     | Ren, F.,                                                                                                                    | PAT 08-OCT-2004                                                           |

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VERSION
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   REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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Chen, J., Feder, J.N., Nelson, T.C., Krystek, S.R. and Duclos, F. Polynucleotides encoding a novel metalloprotease, MP-1
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  Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
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Direct Submission
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   Leiby, K.R., Kapeller-Libermann, R. and Glucksmann, M. 38650, 28472, 5495, 65507, 81588 and 14354 methods of human proteins uses thereof Patent: WO 02074950-A 5 26-527 2002, Millennium Pharmaceuticals, Inc. (US)
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Buteleostomi; Homo.

PAT

22-MAR-2003

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  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
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Contact: MGC help desk
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AX713716
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
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Generation and initial analysis of more than 15,000 full-length
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Submitted (02-AUG-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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  CDNA Library Preparation: Express Genomics CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94: Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
  Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard J
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AUTHORS
TITLE
  SOURCE
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Contact: MGC help desk
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Tissue Procurement: Marcello Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
   Submitted (14-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  Mus musculus
  Direct Submission
  Mus musculus (house mouse)
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BX930694
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  1 LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle
:::|||||:::||||:::||
   BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection, from a library constructed by Elizabeth Bosch. cDNA was prepared from RNA extracted from limbs, normalised, and poly A-trimmed. EcoRI.NotI cut cDNA was then ligated into the vector: Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host: Escherichia coli DH10B.
   Submitted (29-MAR 2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: chickest@bms.umist.ac.uk
On Apr 1, 2004 this sequence version replaced gi:41631222.
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
  Croning,M.D.R., Davies,R.M., Francis,M.D., Grafham,D.V.,
Hubbard,S.J., Humphray,S.J., Hunt,P.J., Maddison,M., McLaren,S.R.,
Niblett,D., Overton,I.M., Rogers,J., Scott,C.B., Taylor,R.G.,
Tickle,C. and Wilson,S.A.
Direct Submission
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Delop 6.0 , I
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1240
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   GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
  Xgapext
Ygapext
Fgapext
Delext
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| ğX          | ž Z           | 8 X     | ŽŽ                    | <b>3 3</b>                                                                                       | 23                                                               | ₹                     | ₹.                                         | ₹ :                          | 2 3                                                                 | ₹                               | Ž 2                | Ž | 3           | ž Ž       | X D X RES                 |            |                   |                    |                    |                   | O                  |                    |                   | C                    |           |                    |                                          | ი        |                    |                    |          |                     |                    |                    |                    |          |                    | n                  |                    |                                          |                    | a        |                    |          |      |
|-------------|---------------|---------|-----------------------|--------------------------------------------------------------------------------------------------|------------------------------------------------------------------|-----------------------|--------------------------------------------|------------------------------|---------------------------------------------------------------------|---------------------------------|--------------------|---|-------------|-----------|---------------------------|------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|----------------------|-----------|--------------------|------------------------------------------|----------|--------------------|--------------------|----------|---------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|------------------------------------------|--------------------|----------|--------------------|----------|------|
| 17-0        | WO2           | Ното    | haer                  | Cro                                                                                              | coag                                                             | בוכנ                  | insı                                       | auto                         | neu                                                                 | Huma                            | NOV                |   | 05-1        | ABX.      | RESULT 1 ABX70950 ID ABX7 |            | ů                 | 4.4                | 43                 | 4 4               | 40                 | υ<br>6             | 37                | 36 0                 | ω<br>4. π | 33                 | 32                                       | 30       | 29                 | 27                 | 26       | 25                  | 2 23               | 22                 | 21                 | 19       | 18                 | 17                 | 15                 | 14                                       | 12                 | 11       |                    | ω        | ٠.   |
| 17-OCT-2002 | WO200281731-A | sapiens | haemostatic;          | Crohn's disease;                                                                                 | coagulation disorder; cancer;                                    | er; burn              | ılin-dep                                   | autoimmune disease; systemic | rodegene                                                            | in; gene                        | Novel human        |   | 05-MAR-2003 | ABX70950; | 70950                     |            | 213               | 213                | 214                | 217               | 224                | 224                | 229               | 231                  | 231       | 231                | 232                                      | 232      | 234                | 239                | 241      | 247                 | 248.5              | 248.5              | 248.5              | 257      | 322                | 332<br>5<br>5      | 468                | 468                                      | 870                | 995.5    | 1059               | 1203     | 1600 |
| •           | -A2,          | Ġ.      | anti                  | ease;                                                                                            | disor                                                            | ; bone                | endent                                     | diseas                       | rative                                                              | 188;                            |                    |   | (first      |           | andard                    |            | 17.2              | •                  | 17.3               |                   |                    | 18.1               |                   |                      | •         |                    |                                          | •        | 18.9               |                    | ٠        | 19.9                | •                  |                    |                    | •        |                    |                    | 37.7               |                                          | •                  |          |                    | 7        | :    |
|             |               |         | iinflammatory;        | anaphylaxis;                                                                                     | der; ca                                                          | disord                | diabet                                     | e; syst                      | diseas                                                              | nervous                         | CUNA sequence #175 |   | st entry)   |           | standard; cDNA; 1416      |            | 1014              | 1014               | 1044               | 9967              | 110000             | 1029               | 1026              | 1206                 | 1026      | 1026               | 1026                                     | 1705     | 300                | 4360               | 1032     | 1053                | 94750              | 1044               | 1000               | 1146     | 1557               | 7691<br>1601       | 371                | 371                                      | 1572               | 3358     | 2208               | 1821     |      |
|             |               |         | ator                  | eixia<br>11                                                                                      | ncer                                                             | er;                   | es n                                       | emic,                        | your<br>Pour                                                        | sys                             | e<br>#             |   | ঽ           |           | 141                       |            |                   |                    |                    | . L<br>. 3        | N 0                |                    |                   | ##                   | 10        | ω.                 |                                          |          |                    |                    |          | N                   |                    |                    |                    |          |                    |                    | 121                | N                                        |                    | 0        | o o                | 0        | •    |
|             |               |         | y; expressed sequence | <pre>anaphylaxis; proliferation; chemotactic;<br/>stem cell growth factor: haematopoiesis;</pre> | coagulation disorder; cancer; tumour; inflammatory disease; sept | osteoporosis; osteoar | ellitus; anaemia; thr                      | lupus erythematosus;         | neurodecenerative disease: Parkinson's disease: Alzheimer's disease | ous system disorder; peripheral | 75.                |   |             |           | 6 BP.                     | ALIGNMENTS | HCHOITOI          | AAS56045           | ABL08591           | ADT05493          | AAT42063_05        | AAS53309           | ADG73343          | ABD02280<br>ABD02197 | ADG73341  | ACA42146           | AAS54064                                 | ААН08019 | AAA00934           | AAD48239           | ACA43173 | ADL03120            | AAF28551           | ACA39102           | ABK37804           | ACA26804 | AAC38454           | ABL24633           | ADL86726           | AAS84622<br>ADL86725                     | ABQ75508           | ADE31345 | ADA52832           | ABS57020 |      |
|             |               |         |                       | notactic; .                                                                                      | ry disease; septic shock;                                        | , ~                   | llitus; anaemia; thrombocytopaenia; wound; | ᄄ.                           | lzheimer's disease:                                                 | eral neuropathy;                |                    |   |             |           |                           |            | ACASIASI FIORALYO | Aas56045 Salmonell | Abl08591 Drosophil | Adt05493 Haemophi | Continuation (6 of | Aas53309 Haemophil | Adg73343 P aerugi | Abd02197 Pseudomon   |           | Aca42146 Prokaryot | Aanibilo Human con<br>Aas54064 Pseudomon | Human    | Aaa00934 Human col | Aad48239 Ehrlichia |          | Addl03120 DNA encod | Aaf28551 Genomic f | Aca39102 Prokaryot | Abk37804 DNA seque |          | Aac38454 Arabidops | Abl24633 Drosophil | Ad186726 DNA up-re | Ads84622 DNA encod<br>Adl86725 DNA up-re | Abq75508 Murine si | Human    | Ada52832 Human cod | CDNA e   | man  |

Result No.

Query Match

Length

DB

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100.0 100.0 100.0

ABX70950 ABS76639 ABA93268 ABS76635 ABS723207

Abx70950 | Ab876639 | Aba93268 | Aba936635 | Abt23207 |

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Human O-s
DNA encod Human pro

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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  Query
DB:
   Percent Similarity:
Best Local Similarity:
  CC Alzheimer's disease; autolimmune disease (e.g. systemic lugus (erythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus) (c) imperiod or lymphoid cell disorders (e.g. anaemia and thrombocytopaemia) (c) wounds, ulcers, burns; bone disorders (e.g. osteoporosis, osteoarthritis); mechanical and traumatic disorders (e.g. stroke, head (c) traumal; lung or liver fibrosis; reperfusion injury in various tissues; (c) bacterial, viral or fungal infections; allergic conditions such as (c) cancer and tumours; and inflammatory diseases (e.g. septic shock, Crohn's (e) disease, anaphylaxis). The protein may be used to inhibit the growth, (c) infection or function of infectious agents such as bacteria, fungi, (c) viruses, or to effect bodily characteristics, biorhythms or circadian (c) cycles of rhythms. The protein may also have (c) proliferation/differentiation, stem cell growth factor, haematopoiesis (c) proliferation/differentiation, stem cell growth factor, haematopoiesis (c) cactivities. The cDNA sequences of the invention are useful for expressing recombinant protein for analysis. The present sequence represents a novel human cDNA sequence of the invention, this sequence is an expressed condition of the invention are useful for expressing conditions.
   밁
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  Alignment Scores: Pred. No.:
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   This invention relates to the cDNA sequences encoding an isolated novel human polypeptide. The protein encoded by the mucleic acid of the invention is useful for treating central and peripheral nervous system diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic lateral sclerosis), neurodegenerative diseases (e.g. Parkinson's disease,
  Novel polypeptide useful for treating neurodegenerative diseases, my or lymphoid cell disorders, bone disorders, mechanical and traumatic disorders, coagulation disorders, and inflammatory diseases.
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Conservative:
Mismatches:
Indels:
Gaps:
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Wang
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  Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; fimmune disease; Theumatoid arthritis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia; emphysema; cystic fibrosis; vascular disorder; inflammatory disorder;
                          New isolated nucleic acid entreating, or ameliorating dimetalloproteinase activity,
  05-FEB-2001;
10-APR-2001;
   05-FEB-2002; 2002WO-US003353
  Homo
  DNA encoding novel human metalloprotease MP1 fragment
  ABS76639;
   ABS76639
  P-PSDB;
  19-SEP-2002
  neurological disorder; gene; ds.
   11-DEC-2002
   (BRIM )
   1246
  1186
  1126
  1066
   1006
   2002-723329/78.
  sapiens.
   221
   201
   181
  161
  141
   946
   121
   988
   101
  826
  ABG96487
   BRISTOL-MYERS
   ATATCAAAAGAAGTTGGAGAAGCTTCCATAAAAGTACCACAATTAAAAAATGGAGATA 1302
   IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle
  GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp
  GlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg
  HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro
   GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys
  Feder J,
   standard; DNA; 1526
  GGCATTTTACATGACATAGAAGGCATCCGCTATGAACCAAAATGTCCTCTTGGAGTAGAC 1245
  TGCACTGATAATGGCATTATGATTGCATGGAATGGTATTGAAAGACTACGTGCTGGCTTG 1185
   CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu
   GCTCTGGAAATTTTAACAAACGCAACACAGTGCACTTTGTTGTGTCCTCCCCAGACTA 1125
   AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu
  CAAAATAATGCAGTACTGGTTGCATCTGGTGGTGTCGCAAGTAACTTCTATATCCGCAGA 1065
   CATCTTGTGAAAAGAACACATCGGGCTATTCTGTTTTGTAAGCAGAGACATTGTTACCT
  CTTCAACACGTTACTGATAAAATAATAATGAAAAAGGAAAAAAGAGGAAGGTATTGAGAAG
  2001US-0266518P
2001US-0282814P
   (first entry)
  Nelson
   SQUIBB
  encoding MP-1 protein, useful for preventing diseases associated with aberrant
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                            e.g.
  8
   Duclos
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A
                                  metabolic,
  #1.
                            , and
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  1005
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   885
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   140
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neurological

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Best Local Si
Query Match:
DB:
   Alignment
Pred. No.:
  US-10-649-273-2_COPY_176_414 (1-239)
  Percent Similarity:
Best Local Similarity:
   The invention describes an isolated nucleic acid molecule (I) encoding a CC metalloprotease (MP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder, an aberrant glutamate transport or motor neuron disorder, such as CC amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like CC condition. The compositions and methods are also useful for diagnosing, CC prognosticating, treating, ameliorating and/or treating disorders CC associated with MP-1 activity, e.g. diabetes, cancer, reproductive disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell caplasia), metabolic disorders (e.g. premature puberty, Kallman syndrome, CC or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, Parkinson's disease, Huntington's disease or Tourette syndrome), liver and renal diseases and immune disorders (e.g. Alzheimer's disease; CC and renal diseases and immune disorders (e.g. Alzheimer's disease or Parkinson's disease). This sequence represents a CC Alzheimer's disease or Parkinson's disease). This sequence represents a metabloprotease MP1 polynucleotide
  Disclosure; Page 462-463; 473pp; English.
  Sequence 1526 BP; 484 A; 297
   No.:
  565
   505
  445
  385
   325
  625
  101
   161
   141
  121
   101
  265
   205
   145
   81
  61
  41
   21
  _
   GlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg
  HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro 140
  GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys 120
   AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu
  LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuGlyLysSerLeuAspIle
CysTillaspāsnGiyIiemetlieAiaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu 200
   AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu
  HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
   CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe
   CATCTTGTGAAAAGAACACATCCGGCTATTCTGTTTTGTAAGCAGAGAGACTTGTTACCT
  LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys 100
  CTGTTGGCATTAGTTCAAGGAGTTTCAGATTTTCTGCTTCTTGGAAAGTCTTTGGACATA 144
   CTTCAACACGTTACTGATAAAATAATAATGAAAAAGGAAAAAGAGGAAGGTATTGAGAAG
   TGCTCCACCATGAGTGGTGGGAAAGCCATAGAACATTTGGCCAAACAAGGAAATAGATTT
   3.57e-132
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  x ABS76639 (1-1526)
  289
  Conservative: Mismatches: Indels:
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  1526
239
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  0 Other;
   180
   564
   160
  324
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  624
  504
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   384
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
   RESULT 3
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JID ABA93268
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  US-10-649-273-2_COPY_176_414 (1-239)
   Alignment
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   Score:
  Pred. No.:
   The present sequence encodes human O-sialoglycoproteinase-like protein (OSGPLP). The present invention also describes: (1) the preparation of the OSGPLP protein; (2) applying the OSGPLP protein in diagnosis; (3) the prevention and/or treatment of related diseases; (4) utilising the OSGPLP protein in screening its agonist, excitomotor and inhibitor and preparing an antibody against the OSGPLP protein; and (5) the use of the OSGPLP polynucleotide sequences, proteins, agonists, excitomotors, inhibitors and antibodies in treating diseases related to the abnormal OSGPLP gene and in preparing the medicine composite for the treatment
   O-sialogycoproteinase-like protein and encoding polynucleotide, useful for diagnosing, preventing and treating related diseases.
  ABA93268
  Sequence 2058 BP;
   Claim 5; Page 29-30 (Disclosure); 38pp; Chinese.
   19-APR-2000;
   19-APR-2000;
  24-OCT-2001
  CN1318550-A.
  Homo
   Human O-sialoglycoproteinase-like protein encoding
   19-APR-2002
  ABA93268;
  (SHAN-)
   sapiens.
635
  745
  221
   685
  201 GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp
  O-sialoglycoproteinase-like
   SHANGHAI SHENGYUAN GENE DEV CO LTD.
LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle
  | IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 239
  ATATCAAAAGAAGTTGGAGAAGCTTCCATAAAAGTACCACAATTAAAAATGGAGATA 801
   GGCATTTTACATGACATAGAAGGCATCCGCTATGAACCAAAATGTCCTCTTGGAGTAGAC
   2000CN-00106834.
   2000CN-00106834.
   (first
   110. .1354
   /product= "O-sialoglycoproteinase-like
  *tag=
  Location/Qualifiers
  637 A; 400
   5.45e-132
1240.00
100.00%
100.00%
100.00%
   cDNA;
   entry)
   2058
  ü
   ВP
  x ABA93268 (1-2058)
  410 G; 611 T; 0 U; 0 Other;
  Conservative: Mismatches: Indels:
  Gaps:
  Length:
Matches:
  protein;
   OSGPLP;
  2058
239
0
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0
   CDNA SEQ ID NO:1.
  enzyme; gene; ss
  protein"
     694
   20
   744
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   RESULT 4
   Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Cushing's syndrome; neurodegenerative disease; Tourette syndrome; sepsis; liver disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; jimmune disorder; rheumatoid arthrittis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia.emphysema; cystic fibrosis; vascular disorder; inflammatory disorder; neurological disorder; gene; ds.
                    05-FEB-2002; 2002WO-US003353
   19-SEP-2002.
   Homo sapiens
  DNA encoding novel human metalloprotease MP1.
   ABS76635
  1295
  1115
  1055
  1175
  1235
   181
   161
   995
   201
  141
   121
   935
  101
  695
  755
  81,
  13
   41
   21
   HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro
  ATATCAAAAGAAGTTGGAGAAGCTTCCATAAAAGTACCACAATTAAAAATGGAGATA 1351
   GlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg
  GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys
  HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
  CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe
   IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 239
  GGCATTTTACATGACATAGAAGGCATCCGCTATGAACCAAAATGTCCTCTTGGAGTAGAC
   GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp
  GCTCTGGAAATTTTAACAAACGCAACACAGTGCACTTTGTTGTGTCCTCCTCCCAGACTA
  AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu 180
  CAAAATAATGCAGTACTGGTTGCATCTGGTGGTGTCGCAAGTAACTTCTATATCCGCAGA
  CATCTTGTGAAAAGAACACATCGGGCTATTCTGTTTTGTAAGCAGAGAGACTTGTTACCT
   CTTCAACACGTTACTGATAAAATAATAATGAAAAAGGGAAAAAGAGGAAGGTATTGAGAAG
  LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys
  TGCTCCACCATGAGTGGGGAAAGCCATAGAACATTTGGCCAAACAAGGAAATAGATTT
  AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu
   (first entry)
   DNA;
   2197
   BP
   pneumonia;
  1234
   200
  1174
  1114
  140
  100
   1054
  160
   874
   814
   60
   934
  90
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CC metalloprotease (MP-1). (I) is useful for preventing, treating, or cc ameliorating a medical condition, particularly an immune disorder, an cc aberrant glutamate transport or motor neuron disorder, such as cc amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like cc condition. The compositions and methods are also useful for diagnosing, cc prognosticating, treating, ameliorating and/or treating disorders (CC associated with MP-1 activity, e.g. diabetes, cancer, reproductive (CC disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell aplasia), metabolic disorders (e.g. premature puberty, Kallman syndrome, cc or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, Huntington's disease or Tourette syndrome), liver cand renal diseases and immune disorders (e.g. AIDS, rheumatoid arthritis (CC or sepsis), pulmonary diseases (e.g. pneumonia, emphysema or cystic (Alzheimer's disease or Parkinson's disease). This sequence represents a cc metalloprotease MP1 polynucleotide
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  US-10-649-273-2_COPY_176_414 (1-239) x ABS76635 (1-2197)
   Query Match:
DB:
  Percent Similarity:
Best Local Similarity:
  Score:
   Alignment
  New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and
  Sequence 2197
  Claim 1;
  neurological disorders.
   05-FEB-2001; 2001US-0266518P.
10-APR-2001; 2001US-0282814P.
   No.:
   (BRIM )
   2002-723329/78.
)B; ABG96478.
               101
   996
   936
  876
   816
  756
  81
   61
  41
   21
GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMctAlaCys
  LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGlyIleGluLys
   HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
  CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe
   AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu
  CTGTTGGCATTAGTTCAAGGAGTTTCAGATTTTCTGCTTCTTGGAAAGTCTTTGGACATA
  LeuLeuAlaLeuValGinGlyValSerAspPheLeuLeuGlyLy8SerLeuAspIle
   Fig 1A-C; 473pp; English.
   CATTTTGACATCAAACCTCCCTTGCATCATGCTAAAAATTGTGATTTTTCTTTTACTGGA
  TGCTCCACCATGAGTGGTGGGAAAGCCATAGAACATTTGGCCCAAACAAGGAAATAGATTT
   CTTCAACACGTTACTGATAAAATAATAATGAAAAAGGAAAAAAGGGAAGGTATTGAGAAG
  BP; 681 A; 441 C; 439
  5.98e-132
1240.00
100.00%
100.00%
100.00%
  Nelson
   SQUIBB
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   8
  Duclos F,
  Conservative: Mismatches: Indels:
  Length:
Matches:
   Gaps:
  G; 636
  Krystek
  T; 0 U; 0 Other;
  S
  100
  815
   80
  935
  60
   875
   40
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정 유

121

HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro

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RESULT 5
ABT23207
      22-JUN-2001; 2001US-0300508P.
06-JUL-2001; 2001US-0303445P.
11-JUL-2001; 2001US-0305405P.
09-AUG-2001; 2001US-0311442P.
24-AUG-2001; 2001US-0318921P.
29-AUG-2001; 2001US-0315992P.
03-MAY-2002; 2002US-0378205P.
   Gandhi AR, Kable AE, Swarnakar A, Hafalia AJA, Tran B, Duggan BM; Warren BA, Ison CH, Honchell CD, Nguyen DB, Lu DAM, Lee EA, Yue I Forsythe IJ, Barroso I, Ramkumar J, Griffin JA, Li JX, Yang J; Thangavelu K, Gietzen KJ, Ding L, Baughn MR, Borowsky ML, Yao MG; Walia NK, Mason PM, Gururajan R, Lee S, Becha SD, Lee Sy, Tran UI Billiott VS, Luo W, Sprague WW, Tang YT, Lu Y, Zebarjadian Y;
   Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; anticonvulsant; cerebroprotective; antiparkinsonian; nootropic; antiinflammatory; antiulcer; hepatotropic; gynaecological; antibacterial; virucide; protozoacide; antiparasitic; cell proliferative disease; PMOD; protein modification and maintenance molecule; immunogenic fragment; cancer; autoimmune; inflammatory disease; neurological disorder; gastrointestinal; developmental; vesicle trafficking disorder; infection; protein protein interaction; drug-target interaction;
New isolated human PMOD polypeptide and polynucleotide, useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis
   03-JAN-2003
   WO2003000844-A2
   Homo
   Human protein modification + maintenance molecule DNA SEQ ID No
  ABT23207 standard;
  18-JUN-2002; 2002WO-US019360
  1296
   1236
  2003-184039/18.
  expression
   181
   161
  141
   INCYTE
   IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 239
  CATCTTGTGAAAAGAACACATCGGGCTATTCTGTTTTGTAAGCAGAGAGACTTGTTACCT 1175
   GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp 220
  AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu 180
  CAMMATAMTGCAGTACTGGTTGCATCTGGTGGTGTCGCAMGTAMCTTCTATATCCGCAGA 1235
   GlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg 160
   CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu 200
   GCTCTGGAAATTTTAACAAACGCAACACAGTGCACTTTGTTGTGTCCTCCCCAGACTA 1295
  GGCATTTTACATGACATAGAAGGCATCCGCTATGAACCAAAATGTCCTCTTGGAGTAGAC 1415
  TGCACTGATAATGGCATTATGATTGCATGGAATGGTATTGAAAGACTACGTGCTGGCTTG 1355
  (first entry)
   GENOMICS INC.
  profile; human; gene; ds.
  DNA;
  Ģ,
      and
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:

7.47e-132 1240.00 100.00% 100.00% 100.00%

Conservative: Mismatches: Indels: Length: Matches:

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The invention relates to an isolated polypeptide comprising: any of 28 CC sequences of 48-1256 amino acids; a natural amino acid sequence at least CC 90% identical to the 28 amino acid sequence, 94% identical to a sequence CC of 703 or 267 amino acids, 96% identical to a sequence of 414 amino CC acids, or 97% identical to a sequence of 422 amino acids, all given in CC the specification; or a biologically active or immunogenic fragment of CC in diagnosing, treating and preventing diseases or conditions associated CC with the decreased expression of protein modification and maintenance CC molecules (PMOD), such as cell proliferative diseases (e.g. cancer, CC allergies), neurological disorders (e.g. stroke, Parkinson's disease, CC epilepsy), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g. cendometriosis), developmental, versicle trafficking disorders, and CC infections (e.g. bacterial, viral, parasitic, protozocal). These are also CC useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of PMOD. The PMOD or its or antagonist of the polypeptides, or in altering the expression of the activity of the polypeptides. The microarray is useful in monitoring CC measuring protein.protein interactions, drug-target interactions, and CC encoding a human PMOD protein of the invention
   Claim 91; Page 211; 225pp; English
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2572 BP; 780 A; 489 ü 509 <u>ი</u> 794 ij, 0 U; 0 Other;

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  121
  969
  849
   101
   909
   789
  729
   669
   41
   81
  61
   21 AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu
   1 LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle
GlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg
  GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys
  HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro
  HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
   CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe 60
   LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGlyIleGluLys 100
   CTGTTGGCATTAGTTCAAGGAGTTTCAGATTTTCTGCTTCTTGGAAAGTCTTTGGACATA
   CTTCAACACGTTACTGATAAAATAATAATGAAAAAGGAAAAAGGGAAAGGTATTGAGAAG
   1088
  140
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            The present invention relates to novel 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules which encode adenosine deaminase, glycoprotease or seven transmembrane domain (7TM) receptor family members.
  Human; adenosine deaminase; seven transmembrane domain receptor; cancer; 7TM; glycoprotease; immune disorder; IgA deficiency; allergy; arrhythmia; rheumatoid arthritis; diabetes; atherosclerosis; cardiovascular disorder; hypertension; ischaemic heart disease; obesity; myocardial infarction; endothelial cell disorder; Grave's disease; psoriasis; brain disorder; Parkinson's disease; Alzheimer's disease; haematopoietic disorder; cerebral oedema; metabolic disorder; liver disorder; platelet disorder; chromosome mapping; tissue typing; gene therapy; neuroprotective; cytostatic; anorectic; cardiant; haemostatic; gene; ss.
  New 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules, useful for diagnosing and treating cancer, immune, cardiovascular, hematopoietic, brain, pain, metabolic, liver or platelet disorders, a
   08-NOV-2000; 2000US-0246768P.
08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
  Claim 1;
  08-NOV-2001; 2001WO-US051427
  WO200274960-A2
  Leiby
   (MILL-) MILLENNIUM
  27-JAN-2003
   AAD46856
  AAD46856 standard;
   1329
  1269
   1149
  1209
   2002-759898/82.
   sapiens.
  181
   161
   221
   201
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   glycoprotease 28472 cDNA.
  AAE29234
  Fig
  IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 239
  GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp
   CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu 200
  AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu
  GCTCTGGAAATTTTAACAAACGCAACACAGTGCACTTTGTTGTGTCCTCCTCCCAGACTA
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  Kapeller-Libermann
  8; 178pp;
  (first
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6 in claim 1 of the specification"
invention are useful in diagnosing
   Cocation/Qualifiers
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   PHARM INC
  CDNA;
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  ВP
  Glucksmann
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  1208
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   Percent Similarity:
Best Local Similarity:
Query Match:
   US-10-649-273-2_COPY_176_414 (1-239)
  or aberrant cellular proliferation and/or differentiation (e.g. colon or lung cancer), immune disorders (e.g. selective IgA deficiency, rheumatoid arthritis, diabetes, allergy), heart or cardiovascular disorders (e.g., hypertension, atherosclerosis, arrhythmias, ischaemic heart disease, myocardial infarction, thrombus) including endothelial cell disorders (e.g. psoriasis, Grave's disease), haematopoietic disorders, brain disorders (e.g. cerebral oedema, Parkinson's or Alzheimer's disease), pain and metabolic disorders (e.g. obesity), liver disorders or platelet disorders. They are also useful in screening assays, predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenetics) and prophylactic and therapeutic methods. The nucleic acids may also be used in chromosome mapping, tissue typing and forensic biology and as surrogate markers. Sequences of the invention are also used in gene therapy. The present sequence is human glycoprotease
   Sequence 1820
   No.:
  1211
  1151
   1091
  1031
   181
   141
   971
  161
  121
   101
  911
   851
   791
  731
  61
   41
   81
  21
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   GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys
   LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys
  CATTITIGACATCAAACCTCCCTTGCATCATGCTAAAAATTGTGATTTTTCTTTTACTGGA
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  CAAAATAATGCAGTACTGGTTGCATCTGGTGGTGTCGCAAGTAACTTCTATATCCGCAGA
  CATCTTGTGAAAAGAACACATCGGGCTATTCTGTTTTGTAAGCAGAGAGACTTGTTACCT
   GGGCAAATCCTGTCTTCAGCAGCAGACATTGCTGCCACAGTACAGCACACAATGGCATGT
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  BP;
   543 A; 365
  8.22e-128
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98.33%
97.07%
97.02%
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  x AAD46856 (1-1820)
  393
   Conservative: Mismatches: Indels:
  Length:
Matches:
  Gaps:
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  518
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  U; 1 Other;
   1330
   1150
  1270
  1210
  180
  1090
   1030
  120
                              220
   200
   160
  140
  970
   100
  910
   80
   850
   60
  790
   40
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IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle

239

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CC deaminase), 28472 (encoding a glycoprotease), 5495 (encoding a 7) CC transmembrane receptor), 65507, 81588 or 14354 nucleic acid molecule (or CC a sequence which is at least 60% identical to the six nucleic acids or CC their open reading frames, fragments of at least 15 nucleotides or CC their open reading frames, fragments of at least 15 nucleotides or CC with the American Type Culture Collection as Accession No. not defined in CC the specification, which encodes the amino acid sequence). Also included CC are a host cell containing the nucleic acids (used to produce the proteins), the encoded proteins, an antibody that selectively binds to CC the polypeptide, and identifying a compound that binds to/modulates the CC activity of the polypeptide. The nucleic acid molecules, polypeptides and CC methods are useful for diagnosing, treating cancer, aberrant cellular CC proliferation and/or differentiation, immune disorders, heart disorders, CC cardiovascular disorders including endothelial cell disorders, main CC ind matabolic disorders, blood vessel disorders, brain disorders, pain CC camples of these disorders are given in the specification). The present CC sequence is the Human CDNA 28472 encoding a glycoprotease
  New isolated 38650, 28472, 5495, 65507, 81588 and 14354 nucleic acid molecules, useful for diagnosing, treating cancer, pain, or immune, heart, endothelial cell, hematopoeitic, blood vessel, brain, metabolic
   CDS
   Human; ss; gene; cancer; aberrant cellular proliferation; differentiation; immune disorders; heart disorder; brain disorder; cardiovascular disorder; endothelial cell disorder; pain disorder; haematopoeitic disorder; blood vessel disorder; metabolic disorder; liver disorder; platelet disorder; glycoprotease.
  The invention relates to an isolated 38650 (encoding adenosine
  Claim
   08-NOV-2000;
08-NOV-2000;
   08-NOV-2001; 2001US-00012140
  08-JUL-2003
   ACA60887;
   Leiby
   (LEIB/) LEIBY K R.
(KAPE/) KAPELLER-LIBERMANN
(GLUC/) GLUCKSMANN M A.
  US2003009017-A1.
  Homo sapiens.
  15-NOV-2000;
  2003-428888/40
  ABU09569.
   Fig 8; 90pp; English.
  standard; cDNA; 1820
   Kapeller-Libermann
  28472 encoding a glycoprotease
   2000US-0246768P.
2000US-0246772P.
2000US-0249185P.
   146. .1390
   /product= "Glycoprotease"
/note= "This CDS is specifically
  Location/Qualifiers
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   Glucksmann
   claimed
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   US-10-649-273-2_COPY_176_414 (1-239)
  Alignment
Cancer; aberrant cell proliferation; aberrant cell differentiation; breast cancer; ovarian cancer; prostate cancer; colon cancer; lung cancer; immune disorder; heart disorder; cardiovascular disorder;
  Sequence 1820
   chia encoding
  30-JAN-2003
  ABS57020;
  ABS57020
  No.:
   1091
  1271
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  1151
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  731
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  ATATCAAAAGAAGTTGGAGAAGCTTCCATAAAAGTACCACAATTAAAAAATGGAGATA 1387
  IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 239
  GGCATTTTACATGACATAGAAGGCATCCGCTATGAACCAAAATGTCCTCTTGGAGTAGAC 1330
   GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp
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   GlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg
   CATCTTGTGAAAAGAACACATCGGGCTATTCTGTTTTGTAAGCAGAGAGACTTGTTACCT 1090
  HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro
   GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys 120
  LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGlyIleGluLys
   CATTITGACATCAAACCTCCCTTGCATCATGCTAAAAATTGTGATTTTTCTTTTACTGGA
   HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
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   CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe
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   LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle
   TGCACTGATAATGGCATTATGATTGCATGGAATGGTATTGAAAGACTACGTGCTGGCTTG 1270
  GCTCTGGAAATTTTAACAAACGCAACACAGTGCACTTTGTTGTGTCCTCCCCAGACTA
   CTTCAACACGTTACTGATAAAAATAATGAAAACAGGAAACAAGAGGAAGGTATTGAGAAG
  (first
  BP;
  novel human glycoprotease 28472
  543 A; 365
   8.22e-128
1203.00
98.33%
97.07%
97.02%
  CDNA; 1821
  entry)
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Matches:
Conservative:
  ACA60887
   Mismatches:
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  518 T; 0
  (1-1820)
  1820
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  U; 1 Other;
  1210
  160
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   970
  910
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   850
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Best Local Similarity:
Query Match:
DB:
   Score:
   The invention describes isolated 38650, 28472, 5495, 65507, 81588 and CC 14354 nucleic acid molecules (I) and their encoded polypeptides (II). The CS 38550 nucleic acid molecule comprises a sequence encoding adenosine CC deaminase. The 28472 nucleic acid molecule comprises a sequence encoding recoding adenosine CC deaminase. The 28472 nucleic acid molecule comprises are comprises as equence encoding adenosine CC sequences that encode a human seven transmembrane domain (7TM). The CC 38550, 28472, 5495, 65507, 81588 and 14354 comprise CC sequences are useful for diagnosing, preventing or treating a subject CC with or at risk of developing a disorder, e.g. cancer or aberrant CC cellular proliferation and/or differentiation (e.g. breast, ovarian, CC prostate, colon or lung cancer), immune disorders, heart disorders, CC cardiovascular disorders, endothelial disorders, heart disorders, CC cardiovascular disorders, brain disorders, pain and metabolic disorders, CC liver disorders or platelet disorders, pain and metabolic disorders, CC liver disorders or platelet disorders, autoimmune disorders, CC ischaemia, Hodgkin's disease, autoimmune disorders, CC ischaemia, heart disease, Crohn's disease, Grave's disease, Kawasaki CC syndrome, Raynaud's disease, aneurysm, cerebral ischaemia, peripheral cc carchexia or diabetes. This sequence encodes the novel human glycoprotease CC Cachexia or diabetes. This sequence encodes the novel human glycoprotease CC Cachexia or diabetes. This sequence encodes the novel human glycoprotease
   Percent Similarity:
   endothelial disorder; hematopoietic disorder; blood vessel disorder; brain disorder; pain; metabolic disorder; liver disorder; diabetes; platelet disorder; carcinoma; sarcoma; leukaemia; Hodgkin's disease; autoimmune disorder; hypertension; atherosclerosis; heart failure; myocardial infarction; ischaemic heart disease; Crohn's disease; Grave's disease; Kawasaki syndrome; Raynaud's disease; aneurysm; cerebral ischaemia; peripheral neuropathy; Alzheimer's disease;
  New adenosine deaminase, glycoprotease and nucleic acids and polypeptides, designated 81588 and 14354, useful for treating e.g. 1
  08-NOV-2000; 2000US-0246768P.
08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
  Key
  Sequence
   WO200277233-A2
   Claim
  Leiby
   08-NOV-2001; 2001WO-US046724.
   Homo
   Parkinson's
   (MILL-) MILLENNIUM PHARM INC.
  No.:
   sapiens.
  2003-029938/02.
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   /*tag= a
/product= "Glycoprotease 28472"
/note= "Specifically claimed in
   Location/Qualifiers
147. .1391
  543
  8.22e-128
1203.00
98.33%
97.07%
97.02%
   178pp;
  anorexia nervosa; cachexia; glycoprotease; gene;
  ð
  365
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  394
Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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  518
   d seven transmembrane
d 38650, 28472, 5495,
leukemias, Hodgkin's
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   claim
  1 Other;
  domain
65507,
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RESULT 9
ADA52813
ID ADA5
XX ADA5
AC ADA5
XX Huma
XX Cytc
KW Gene
KW inf1
XX Homc
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   US-10-649-273-2_COPY_176_414 (1-239) x ABS57020 (1-1821)
  Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease; gene; ss.
                        21-MAR-2002;
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  Human
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  SEQ
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  The present invention relates to novel human secretory or membrane proteins (ADA54712-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
   Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
   24-JAN-2002; 2002US-0350435P
   Хо
::
   polynucleotides encoding full-length polypeptides, e.g. secretory
/or membrane proteins, useful for developing medicines for diseases
ch the gene is involved, or as target molecules for gene therapy.
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   1049
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  2003-395539/38.
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  141
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 181
   989
   929
  698
   81
  61
  41
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RES ASSOC BIOTECHNOLOGY
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  2208
  SEQ ID NO 400; 205pp; English
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88.28%
85.40%
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Gaps:
   Length:
Matches:
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Mismatches:
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  1348
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   988
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5.67e-111 1059.00 88.28% 88.28% 85.40%

Length: Matches:

Score: Pred. No.:

US-10-649-273-2\_COPY\_176\_414 (1-239)

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ADQ24627 Gaps: Mismatches: Indols: Conservative:

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  The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is that of a human soft tissue sarcoma within the specification per se but was submitted in CD format by the inventor.
   Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                           Sequence 2890
   Example 2; SEQ ID NO 7447; 210pp; English.
   WPI; 2004-441208/41.
  26-NOV-2003; 2003WO-US038193
  Homo
  Human soft tissue sarcoma-upregulated DNA -
   Aziz
  26-NOV-2002; 2002US-0429739P
  WO2004048938-A2
   soft tissue
   26-AUG-2004
  ADQ24627;
   ADQ24627
   (PROT-)
  10-JUN-2004
   10
  1409
Scores:
   1457
   1436
   z
   sapiens
   221
   PROTEIN DESIGN LABS INC
  Ginsburg WM,
   standard;
  IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle
   GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp
   ATATCAAAAGAAGTTGGAGAAGCTTCCATAAAAGTACCACAATTAAAAATGGAGATA
  sarcoma; cytostatic; gene therapy; vaccine; screening; human;
  (first
                           BP; 869 A; 609
   DNA;
  entry)
  Zlotnik A;
  2890
                            Ç
  ВP
                            611 G;
                              789
   ----TGATGTCCTCTTGGAGTAGAC 1456
                            T; 0 U; 12 Other;
  SEQ ID 7447
   1513
  239
  220
  1435
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ARESULT 11
ADE31345/c
ID ADE313
XX ADE313
XX ADE313
XX ADE313
XX ADE313
XX DT 29-JAN
XX diagno
XX diagno
XX diagno
XX diagno
XX diagno
XX entiin
XX inmuno
XX osteop
XX viruci
XX viruci
XX gene t
XX gene t
XX young
XX Homo s
XX Homo s
XX Homo s
XX Homo s
XX Homo s
XX Homo s
XX YOLOO3
XX ADE31345/c
  diagnostic and therapeutic polynucleotide; dithp; antiarteriosclerotic; antiinflammatory; cerebroprotective; antilipaemic; antidiabetic; immunosuppressive; neuroprotective; nortropic; neuroleptic; tranquilizer; osteopathic; antiarthritic; antirheumatic; cytostatic; hepatotropic; virucide; haemostatic; anti-HIV; antithyroid; thyromimetic; virucide; antibacterial; fungicide; antiparasitic; anticonvulsant; dermatological; antibacterial; fungicide; antiparasitic; anticonvulsant;
  WO2003062376-A2
  thrombolytic;
  Human diagnostic and therapeutic polynucleotide (dithp), SEQ ID No 100
  29-JAN-2004
   ADE31345
  ADE31345
   1946
   1886
  1706
  1646
  2093
   2006
  1826
  1766
   1586
  181
  161
  141
  121
   101
   81
   61
   41
   21
  μ
   LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle
   IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 239
  GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp
  CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu
|||||||||
   AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu
  GlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg
  HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro
  GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys
   CTTCAACACGTTACTGATAAAATAATGAAAAAGGAAAAAGGAAAGGTATTGAGAAA
  LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys 100
   HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
   CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe
   AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu
  ATATCAAAAGAAGTTGGAGAAGCTTCCATAAAAGTACCACAATTAAAAATGGAGATA
   GCTCTGGAAATTTTAACAAACGCAACACAGTGCACTTTGTTGTGTCCTCCCCAGACTA
   CAAAATAATGCAGTACTGGTTGCATCTGGTGGTGTCGCAAGTAACTTCTGTATCCGCAGA
   CATCTTGTGAAAAGAACACATCGGGCTATTCTGTTTTGTAAGCAGAGACATTGTTACCT
   GGGCAMATCCTGTCTTCAGCAGCAGACATTGCTGCCACAGTACAGCACACAATGGCATGT
  CATTTTGACATCAAACCTCCCTTGCATCATGCTAAAAATTGTGATTTTCCTTTTACTGGA
  TGCTCCACCATGAGTGGTGGGAAAGCCATAGAACATTTGGCCAAACAAGGAAATAGATTT
   GCACCAGGTGACATGCTTGACAAGGTGGCAAGAAGACTTCCTTTAATAAAACATCCAGAG
   CTGTTGGCATTAGTTCAAGGAGTTTCAGATTTTCTGCTTCTTGGAAAGTCTTTGGACATA
   anticoagulant; anorectic; vasotropic; antiulcer; protein replacement therapy; human; gene; ds.
  (first entry)
  DNA;
  ВÞ
   -TGATGTCCTCTTGGAGTAGAC
   220
   2092
  200
  180
  160
   1945
  140
   1885
   120
  1825
  1765
  1705
   1645
   1585
   2113
   2065
   2005
   80
   60
   40
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31-JUL-2003

Percent Similarity: Best Local Similarity:

1.4e-103 995.50 87.82% 87.82% 80.28%

Length:
Matches:
Conservative:
Mismatches:
Indels:

Score: Alignment

No.:

Sequence 3358 BP;

1105 A;

577 Ç

601 G;

1075

<del>|</del> ou;

0 Other

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chemistric polymuclectide (designated dithp). The movel dithp colymuclectide comprises: any of 188 DNA sequences consisting of 195-7798 comparising a naturally occurring polymuclectide consisting of 195-7798 comprising a naturally occurring polymuclectide which is at least 90% cidentical to the dithp polymuclectide or its polymuclectide which is at least 90% cidentical; or an RNA equivalent of any of the polymuclectides mentioned complementary to didnitical; or an RNA equivalent of any of the polymuclectides mentioned combined; or its polymuclectide which is at least 90% cidentical; or an RNA equivalent of any of the polymuclectides mentioned combined; or antiatric polymuclectide mentioned combined; or an RNA equivalent of any of the polymuclectides mentioned combined; or antiatric, antiatric, antiatric, antiatric, antitypoid, thyronimetic, cranquillzer, osteopathic, antiatritic, antixparasitic, anticovering, neuropeotective, nootropic, neuroleptic, cranquillzer, osteopathic, antiatritic, antixparasitic, anticovering the polymuclectide, antiparasitic, anticovering the polymuclectide, antiparasitic, anticovering the polymuclectide, anticovering the polymuclectides or DITHP polymuclectides polypeptide can be used in gene therapy and comparisor polymuclectides or DITHP polymuclectides polymuclectides or DITHP polymuclectides or DITHP polymuclectides polymuclectides or DITHP polymuclectides or DITHP polymuclectides polymuclectides or DITHP polymuclect
   New human diagnostic and therapeutic polynucleotides and polypeptides, useful for diagnosing, treating or preventing e.g. leukemia, brain cancer, atherosclerosis, AIDS, thyroiditis, infections, obesity, strok
   16-JAN-2002; 2002US-0349384P.
17-JAN-2002; 2002US-0349413P.
17-JAN-2002; 2002US-0349946P.
  Claim
  or Alzheimer's.
   P-PSDB;
   Peralta CH,
Kristnam SR,
   13-JAN-2003; 2003WO-US001096.
   (INCY-) INCYTE GENOMICS INC
   2003-636732/60
DB; ADE31156.
  1
  ΑĿ,
  invention.
  L, Dahl CR, Gietzen D. Chinn J, D
Tuason O, Yap PB, Amshey SR, Dam
CH, Lewis SA, Chen A, Marwaha R,
n SR, Kolluru V, Panesar IS;
  SEQ ID NO 100;
   634pp; English.
  Dufour GE,
  TC, Liu
Lan RY,
  E, Jackson JL;
u TF, Gerstin E
, Urashka ME;
  stroke
   田;
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RESULT 12
ABQ75508
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  US-10-649-273-2_COPY_176_414 (1-239) x ADE31345 (1-3358)
  CAPN5; tryptase 4; sialoglycoprotease; enzyme; genetic disease; neurological; neuropsychological; psychotic illness; transgenic animal;
         05-DEC-2001; 2001WO-US046405
   WO200245491-A2
   Mus musculus.
  Murine; mouse; protease; calcium activated neutral protease type 5;
  Murine sialoglycoprotease-like gene sequence SEQ ID NO:7.
  ABQ75508;
   ABQ75508
                            13-JUN-2002.
  1446
   1684
  1744
   2104
  1506
   1566
  1625
   1804
  1864
  1984
   2044
  1924
  223
  203
  183
  163
   143
  123
  103
   97
   88
   89
  48
  29
  ValalaargArgLeuSerLeuIleLysHisProGluCysSerThrMetSerGly-GlyLy-48
   standard;
  ysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 239
  alLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnA 143
   TATTCCTGGATTGTGCCTAAAAATAGCTGCTCATTTCTGCAGGTATTGAGAAGGGGCAAA 1805
  euHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAspIleSerL 223
   snAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuG 163
   GCATCATGCTAAAAATTGTGATTTTTCTTTTACTGGACTTCAACACGTTACTGATAAAAT 1925
  uHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIl
  AGCCATAGAACATTTGGCCAAACAAGGAAATAGATTTCATTTTGACATCAAACCTCCCTT
  spAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleL 203
   luIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeuCysThrA 183
  TGAAAAGAACACCGGGCTATTCTGTTTTGTAAGCAGAGAGACTTGTTACCTCAAAATA 1685
   TCCTGTCTTCAGCAGCAGACATTGCTGCCACACAGTACAGCACAATGGCATGTCATCTTG 1745
  leLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuV 123
   AATAATGAAAAAGGAAAAAGAGGAAGGTATATTTCTAATTAGTAAAGTTGAACAGATAAA 1865
  sAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLe 68
  AAATTTTAAC-AACGCAACACAGTGCACTTTGTTGTGTCCTCCCCAGACTATGCACTG
  ATGCAGTACTGGTTGCATCTGT-GGTGTCGCAAGTAACTTCTATATCCGCAGAGCTCTGG
   (first
  -GlyIleGluLysGlyGlnI
   1397
  1507
  1567
  1626
  103
   1985
   88
  2045
   96
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Sequence 1572 BP;

459 A; 337 C;

340 G; 429

T; 0

U; 7 Other;

Query Match: DB: US-10-649-273-2\_COPY\_176\_414 (1-239) Best Local Similarity: Percent Similarity: 648 588 528 708 81 61 41 21 1 LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlvIleGluLys CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe CIGTIGGMRITAGICCAAGGIGITICCGATTICCIGCICCTIGGGAAGICTITGGACATA TGTTCTACAATGAGTGGAAAAAGCTATAGAACAGTTGGCCAAAGACGGAAATAGATTC 1.28e-89 870.00 82.77% 77.31% x ABQ75508 Length: Matches: Mismatches: Indels: Conservative: (1-1572)1572 184 13 37 5

101

GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys

120

887

767 100 707

827

60

647

40

587

CTTCAACATATTACTGATAAGCTAATAACACACACAAGGAAAAAGAAGGCATTGAGAAG

768

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          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging
  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
   Claim 1;
  Drmanac
  31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
  30-MAR-2001; 2001WO-US008631
  WO200175067-A2
  Homo
  Human;
  DNA encoding novel human diagnostic protein
   AAS84622
   AAS84622 standard; cDNA;
  WPI;
   11-OCT-2001
  13-FEB-2002
  (HYSE-) HYSEQ INC.
  food
  1127
   1067
   1008
  1187
   n; chromosome mapping; gene mapping; gene therapy; forensic;
supplement; medical imaging; diagnostic; genetic disorder;
  2001-639362/73
)B; ABG20435.
   sapiens
  201
  181
   161
  948
   141
  121
  RT,
   SEQ ID NO
  GİnAsnAsnAlaValLeuValAlaSerGİyGİyValAlaSerAsnPheTyrIleArgArg 160
  HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro
   GGCATTATCCCGAAGAAGTTGGCAGA---AGCTTGCCCCATTAAAAAGTTA
  GlyIleLeu-HisAsp-IleGluGlyIleArgTyrGluProLysCysProLeuGlyVal-
   CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu
  AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu 180
  --AspīleSerLysGluValGlyGluAlaSerIleLysValProGlnLeu 235
  CACCTTGCGAAAAGAACACATCGCGCTATTCTGTTTTGCAAGCAGAAAAATTTGCTCTCT 947
   GCATTGGAAATTGTCGCAAATGCAACGCATGCACGGTTGTTGTGTCCACT-TCAAGACTG
  CCAGCTAACGCAGTATTAGTTGTATCTGGAGGTGTTGCAAGTAACTTGTACATCCGAAAA 1007
   GGCCTTTTACCATGATAGAGACATTCGGTTATTAACCCAAATGTCCTCTTTGAGTGA
  Liu C,
  (first entry)
  20426; 103pp; English.
  Tang
   2734
  ĭ
   ВP
are useful for treating disorders
  #20426
   mutations
  88
  1186
  219
  200
  1126
  1066
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RESULT 14
ADL86725
ID ADL86
XX
AC ADL86
AC ADL86
DT 20-M2
XX
DE DNA V
  문
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   닭
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   US-10-649-273-2_COPY_176_414 (1-239)
  Query Match:
DB:
   Percent Similarity:
Best Local Similarity:
  Alignment Scores:
   involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
  Sequence 2734 BP;
                 DNA up-regulated in
  20-MAY-2004
  ADL86725;
  ADL86725
  No.:
   584
   205
  644
  185
   165
   524
   145
  464
  125
   404
   105
   344
  284 TCTGCTTCTGGGGAGGCCCAGGGAGCTTTTACTCATGGCGAAAGGCAAATTGGGAGTAGG
   236
  206
  87
  43
   63 AspIleLysProProLeuHisHisAlaLys-----AsnCys--
  standard;
  AspIleGluGlyIleArgTyrGluProLys-----CysProLeuGlyVal 219
  GGCATTATGAAATGCATGAATGGTATTGAAAGACTACGTGCTGGCTTGGGCATTTTACAT
   GlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHis
  LeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsn
  GTACTGGTTGCATCTGGTGGTGTCGCAAGTAACTTCTATATCCGCAGAGCTCTGGAAATT
  ValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIle
  AGAACATCGGGCTATTCTGTTTTGTAAGCAGAGAGACTTGTTACCTCAAAATAATGCA
  ArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAla
   TCTTCAGCAGCAGACATTGCTGCCACAGTACAGCACAATGGCATGTCATCTTGTGAAA
  SerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLys
   CGTCTTACATGGCAGGAGCAGGACCGAGAGAGGGGGGGTATTGAGAAGGGGGCAAATCCTG
   LysIleIleMetLysLysGluLysGluGlu-----GlyIleGluLysGlyGlnIleLeu
::::::
  ACCCTGCTAGGGGGCGCCGCT------AGATTCCAT---
   ThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPhe
  GACATAGAAGGCATCCGCTATGAACCAAAGTATGTGGCTCCTTCAGGGCTG
  -----CCTATTTCTCCGATGAAAGTATCAGGCTGTGTAGGAAGCGTGGCAGCA
   (first
  4.02e-58
599.00
71.57%
66.50%
48.31%
  773 A; 545
                 murine multipotent progenitor cells
  entry)
  371
  Ç
  x AAS84622 (1-2734)
   639 G;
   Conservative: Mismatches: Indels:
   Length:
Matches:
   Gaps:
   763
   Ή,
   0
   U; 14
   Other;
                 SeqID
  . . . . . . . . . . . . . .
  754
   204
   184
   523
   144
   463
   124
  104
   343
  62
   643
  583
  164
  403
   98
   74
  235
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Percent Similarity:
Best Local Similarity:
Query Match:
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  US-10-649-273-2_COPY_176_414 (1-239)
   Alignment Scores:
  This invention relates to a novel method for predicting gene potential by associating nucleic acid sequences of unknown function with particular sub-population profiles. Specifically, it refers to classifying an unknown multi-lineage affiliated gene by collecting hybridisation data to develop a gene expression map, in order to determine the discrete sub-population where it is expressed. The present invention describes methods for predicting the lineage commitment of genes associated with the self-renewing haematopoietic (blood) stem cells (HSCs), as well as the nonself renewing multipotent progenitors (MPPs), common lymphoid progenitors (CLPs) and common myeloid progenitors (MPPs), which are collectively referred to as bone marrow stem cells populations. As such, these methods can be used to identify associated multiplineage affiliated genes and hence the underlying molecular mechanisms in physiological haematopoietic development. This polynucleotide sequence is DNA associated with a murine
  Sequence 371 BP; 104 A; 75
  Claim 8; SEQ ID NO 3118; 123pp; English.
  Classifying an unknown multi-lineage affiliated gene comprises isolating expressed nucleic acid sequences from the discrete cell sub-populations.
   gene potential; multi-lineage; cell commitment; haematopoietic stem cell; HSC; multipotent-progenitor; MPP; common lymphoid progenitor; CLP; common myeloid progenitor; CMP; bone marrow stem cell; mouse; murine; ds.
  03-MAY-2002; 2002US-0377383P
   05-MAY-2003; 2003WO-US014114.
  13-NOV-2003
   WO2003093445-A2
   Mus sp
  MPP sub population
  (STOW-) STOWERS INST MEDICAL RES
                                  169
  182
  122
  149
   169
  129
   109 AspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArg
   62
   N
GCATGGAATGGAATTGAANGATTACGTGCNGNCTTNGGCNTTNTACNTGANNTAGAAGAC
                      ThrGlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIle 188
   SerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAla 168
   GCTATTCTGTTTTGCAAGCAGAAATTTGCTCTCTCCAGCTAACGCAGTATTAGTTGTA 121
  AlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAla 148
  GACATTGCTGCTGCGGTACAGCATGCAACAGCGTGCCACCTTGCGAAAAGAACACATCGC
  TCTGGAGGTGTTGCAAGTAACTTGTACATCCGAAAAGCATTGGAAATTGTCGCAAATGCA
  2.75e-44
468.00
78.86%
74.80%
37.74%
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   cells of the invention.
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  84 G;
  x ADL86725 (1-371)
  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
  92
   T; 0 U;
  16 Other;
  371
92
5
26
0
  181
 301
  241
  19
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109

AspIleAlaAlaThrValGlnHisThrMetAlaCYsHisLeuValLysArgThrHisArg

x ADL86726 (1-371)

US-10-649-273-2\_COPY\_176\_414 (1-239)

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Query Match:
DB:
                                Percent Similarity:
Best Local Similarity:
  8
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   Pred. No.:
   닭
  CC This invention relates to a novel method for predicting gene potential by CC associating nucleic acid sequences of unknown function with particular CC sub-population profiles. Specifically, it refers to classifying an CC unknown multi-lineage affiliated gene by collecting hybridisation data to develop a gene expression map, in order to determine the discrete sub-CC compulation where it is expressed. The present invention describes methods CC population where it is expressed. The present invention describes methods CC renewing haematopoietic (blood) stem cells (HSCs), as well as the non-CC self renewing multipotent progenitors (MPPs), common lymphoid progenitors (CLPs) and common myeloid progenitors (CMPs), which are collectively CC referred to as bone marrow stem cells populations. As such, these methods CC can be used to identify associated multi-lineage affiliated genes and CC can be used to identify associated multi-lineage affiliated genes and CC development. This polynucleotide sequence is DNA associated with a murine CC MPP sub population of cells of the invention.
  gene potential; multi-lineage; cell commitment; haematopoietic stem cell; HSC; multipotent progenitor; MPP; common lymphoid progenitor; CLP; common myeloid progenitor; CMP; bone marrow stem cell; mouse; murine; ds.
   Sequence 371
  Claim 8; SEQ ID NO 3119; 123pp; English.
   Classifying an unknown multi-lineage affiliated gene comprises isolating expressed nucleic acid sequences from the discrete cell sub-populations.
   Li L;
  03-MAY-2002; 2002US-0377383P.
   05-MAY-2003; 2003WO-US014114.
   WO2003093445-A2
  DNA up-regulated in murine multipotent progenitor cells SeqID
  ADL86726;
   ADL86726 standard; DNA;
  13-NOV-2003
   20-MAY-2004
   (STOW-)
   362
  229
   302
  209_IleArgTyrGluProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAla
   STOWERS INST MEDICAL RES
   GCCATAAAA
  SerIleLys
   ATCCNNTATGNACCAAAATNTCNTNTTGGAGTAGACATNTCCAGAGAAGTTGCAGAAGCT
   ₿₽;
   (first
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Search completed: February 16, 2005, 13:59:01 Job time : 468.139 secs

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Sequence 1, Appli
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Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 6612, Ap
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| 42325<br>3215                            | 15249<br>3064                            | 15249              | 1101                | 1026              | 1230230          | 1230025          | 1011               | 640681          | 1664976         | 1664976          | 432               | 1663             | 1011               | 1011            | 10974             | 1107                | 1006             | 1006             | 4411529          | 4403765           | 1155               | 3993               | 822               | 1011             | 1008             | 1092                | 1315            | 1032                | 1074                | 2582              |
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| 131,                                     | 102,<br>794,                             | 102                | 155                 | Sequence 1, Appli | μ                | e 1, A           | 161                | ,<br>,          | ۲               |                  | 261,              | 6, Apr           | 21                 | 1,<br>A)        |                   | 1072                | 51,              | ï                | ,1               | Sequence 2, Appli | 147,               | 3985,              | 727               | ω<br>'           |                  |                     | 1, App          |                     | 2341,               | Sequence 503, App |

## ALIGNMENTS

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TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802
CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
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Wang, Jian-Rui
Wang, Dunrui
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   Ren, Feiyan
Zhang, Jie
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Asundi, Vinod
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
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; TITLE OF INVENTION: SPINAL CORD, MP-1
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A NOVEL

METALOPROTEASE HIGHLY

EXPRESSED

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CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
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; NAME/KEY: CDS
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Sequence 21, Application US/10067443

Patent No. 6642041

GENERAL INFORMATION:
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ITILE OF INVENTION: POLYNUCLEOTIDE ENCODING A PITILE OF INVENTION: SPINAL CORD, MP-1

FILE REFERENCE: DO073 NP

CURRENT APPLICATION NUMBER: US/10/067,443

CURRENT FILING DATE: 2002-02-05

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR APPLICATION NUMBER: US 60/262,814

PRIOR FILING DATE: 2001-04-10

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Best Local Similarity:
Query Match:
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; ORGANISM: homo sapiens
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CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
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OTHER INFORMATION: Incyte template
PUBLICATION INFORMATION:
   APPLICANT: Patterson,
APPLICANT: Berg, Kim,
TITLE OF INVENTION: N
   APPLICANT:
  FEATURE:
  TYPE: DNA
ORGANISM: M. catarrhalis
24464 GCCTATGAGCTGCCAAGACCCATGCAGCAT---AAAGGGCTGGATTTTTCGTTCAGTGGC 24520
  24305 ATGCTGGTGCGTGCCGATGGTGTGGGCGTGTATCAGATATTGGGCGAGTCTATCGATGAT 24364
   13520
  210
   191
  21
  1 LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuClyLysSerLeuAspIle
  GCGGTGGGTGAATGCTTTGATAAAACGGCAAAAATGCTCAAACTG----CCCTATCCT--- 24418
   AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu 40
   ACTAAGCCTTCTTCCTTCAGATCTTGGAGCTATTGATTTTATTTTAATGCTTCTTATTTA 1345
  CACTITGTTGTGTCCTCCTCCCAGACTATGCACTGATAATGGCATTATGATTGCATGGTA 13339
                          HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly 80
  CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe
   GCTATGAACCAAAG 13533
  rgTyrGluProLys 214
  GGAATGGTATTGAAAGACTACGTGCTGGCTTGGGCATTTTACATGACATAGAAGGCATCC
   --AsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleA 210
  AGCCACAGGATATACGTGCTTCACTCATAACTATGTAAATATTAATTGCCATTTTATCAT 13399
  SThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrp--
  TGTCGCAAGTAACTTCTATATCCGCAGAGCTCTGGAAATTTTAACAAACGCAACACAGTG 13279
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   3.02e-20
248.50
48.67%
32.30%
20.04%
  Program
   NUCLEOTIDE SEQUENCES
   Chandra
   Robert,
   GGTGGCCCAAATATCGAAAAATTAGCCAAAAACGGCAACCCACAC 24463
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Matches:
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  Mismatches:
Indels:
   Conservative:
   No.
  얶
   6632636
  MORAXELLA CATARRHALIS GENOME
  94750
73
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Percent Similarity:
Best Local Similarity:
Query Match:
   Alignment Scores: Pred. No.:
   US-10-649-273-2_COPY_176_414 (1-239)
   US-09-540-236-806
   Score:
   US-09-540-236-806
   APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARI
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT PILICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 806
  Sequence 806, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
  LENGTH: 1053
TYPE: DNA
ORGANISM: M.catarrhalis
  24886 GACGCTTGGCGTATCGGC 24903
  24521 ATGAAAACCGCCATTCATAATCTCATCAAAGACACACCAAACGCCCAAAGCGACCCC---
   445 ATGCTGGTGCCGATGGTGTGGGCGTGTATCAGATATTGGGCGAGTCCATCGATGAT 504
  181
  41
   21 AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu 40
   81 LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys
   1 LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle
   CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe 60
   IleSerLysGluValGly 226
   GCGGTGGGCGAATGCTTTGATAAAACGGCAAAAATGCTCAAACTG----CCCTATCCT---
   GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp
  CYsThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu
  AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu
  GlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg
  ACTITIGGTCAAAAAATGCACCAAAGCACTACAGATGACAGGCATTCGCCAG--
   HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro
   GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys 120
  TGCACGGATAATGGTGCGATGATCGCCTATGCTGGCTTTTGTCGGCTCAGCTGTGGACAG
   ----GCCACACGAGCAGACATCGCCGCAAGCTTTGAGTATGCGGTGGTGGAT
   -GATGACTTGGC-GGTTCGCTGTATTCC--
  3.22e-23
247.00
46.85%
31.53%
19.92%
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   x US-09-540-236-806 (1-1053)
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Matches:
   Mismatches:
Indels:
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38
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   24781
  160
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   558
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   24885
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  US-10-649-273-2_COPY_176_414 (1-239) x US-09-252-991A-884 (1-1059)
  Percent Similarity:
  Score:
  US-09-252-991A-884/c
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   Alignment Scores:
   US-09-252-991A-884
  APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 884
LENGTH: 1059
TYPE: DNA
TYPE: DNA
TYPE: DNA
   Sequence 884, Application US/09252991A Patent No. 6551795
  GENERAL INFORMATION:
   ORGANISM: Pseudomonas aeruginosa
   Мо.
:
   1042 TATGAT 1047
   766
   161
   121 HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro 140
  18
  61
 22 ProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCys
                                   TTGGTGCGGGTGGACGGTATCGGCCGCTACCAGTTGCTTGGCGAATCGGTGGACGATGCC 562
   HisAsp 205
  GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys 120
   HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
   TCGGATGACTTGGCGGTTCGCTGTATTCCCCGATGGGATATGACGATGCTTTGGTATCGAA 1041
  TGCACGGATAATGGTGCGATGATCGCTTACGCTTGGCTTTTGTCGGCTAAGCCGTGGGCAG
   AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu
   GlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg
  ACTTTGGTCAAAAATGCACCAAGGCACTACAGATGACAGGCATTCGCCAG-----
   LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys 100
  GCCTATGAGCTGCCAAGACCGATGCAGCAT---AAAGGGGCTGGATTTTTCGTTCAGTGGC
  LeuAlaLeuValGlnGlyValSerAspPheLeuLeuGlyLysSerLeuAspIleAla
   CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGly---
   ATGAAAACCGCCATTCATAATCTCATCAAAGACACGCCCAAACGCCCAAAGCGACCCT---
   ----GCCACACGAGCAGACATCGCCGCAAGCTTTGAGTATGCGGTGGTGGAT
   4.81e-21
231.00
49.54%
33.80%
18.63%
   CTGGTGGTCGCAGGGGGGGCGTCTCTGCCAATCAGACGCTACGCCGC
  Conservative: Mismatches: Indels:
  Length:
Matches:
  Gaps:
   1059
73
34
87
22
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   LeuGlyIleLeu
   180
  199
   921
  160
  660
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   Query Match:
   Percent Similarity:
Best Local Similarity:
   US-09-252-991A-801
   US-09-252-991A-801
  RESULT
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  Pred. No.:
  Alignment Scores:
  Score:
   SEQ ID NO 801
LENGTH: 1206
   GENERAL INFORMATION:
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  198
  162
  249
   142
   294
   122
  345
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  402
   462
   510
  84
   82
   62
  42
   2 LeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAla
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US-10-649-273-2_COPY_176_414 (1-239) x US-09-252-991A-801 (1-1206)
   Sequence 801, Application US/09252991A
Patent No. 6551795
   CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
   APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS A
FILE REFERENCE: 107196.136
   ·TYPE: DNA ORGANISM: Pseudomonas aeruginosa
  561 GCCGGCGAAGCCTTCGACAAGACCGCCAAGCTGATCCGCCTG---GGCTATCCC-----
  ThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGly
  LeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeuCys 181
  LeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGln 141
  GlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHis 121
   AAGACCTTTACCCTGAAC---ACCTGGCAGCGTTGCGTCGAGGCCGGCGACGACAGCGAG
   GlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLysGly 101
   PheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeu
   IleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeu 217
   AsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAla 161
   CAG-----ACCCGCTGCGACATCGCCCTGGCGTTCCAGACCGCGGTGGTCGAGACC
   TTCGTGTTCCCGCGGCCGATGACCGATCGCCCCGGCCTGGACTTCAGCTTCAGCGGGCTC
   SerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHis
   --- CAGCATGACGGCCCGGCGATCAGCGTCCAGCCGCGCTGGCCGATG
  CTGCTGATCAAGTGCCGTCGCGCCTTG----AAGCAGACCGGCCTG-----AAG
  5.95e-21
231.00
49.54%
33.80%
18.63%
   -CTGGTGATCGCCGGCGGTGTCAGCGCCCAACCAGGCGCTGCGCAGCGGC 199
   GETGETCCGGAAATCGCCCGCCTGGCGGAGCGCGGCACTCCTGGCCGC
   Length:
Matches:
  Conservative:
Mismatches:
  Indels:
  AND
  SEQUENCES RELATING TO PSEUDOMONAS
  1206
73
34
87
22
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   463
21
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   201
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   250
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   81
  61
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RESULY 17

US-09-557-884-1/c
; Sequence 1, Application US/09557884
; Patent No. 6506581
; PATENT INFORMATION:
; APPLICANT: Fleischmann et al.
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd
            ZIP: 20850

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/557,884

FILING DATE: 25-Apr-2000

CLASSIFICATION: «Unknown»

PRIOR APPLICATION DATA:

AFFLICATION DATA:

AFFLICATION NUMBER: US/476,1U2

FILING DATE: JUN-5-1995

ATTORNEY/AGENT INFORMATION:
   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
  1141 ---CAGCATGACGGCCGGCGATCAGCGTCCAGCCGCCTGGCCGATG 1185
   1087
  1027
   182
  162
   976
   142
  931
  880
  122
  102 GlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHis 121
   823 AAGACCTTTACCCTGAAC---ACCTGGCAGCGTTGCGTCGAGGCCGGCGACGACAGCGAG
   763 TTCGTGTTCCCGCGGCCGATGACCGATCGCCCCGGCCTGGACTTCAGCTTCAGCGGCTC
   664 GCCGGCGAAGCCTTCGACAAGACCGCCAAGCTGATCGGCCTG---GGCTATCCC----- 714
  604 TTGGTGCGGGTGGACGGTATCGGCCGCTACCAGTTGCTTGGCGAATCGGTGGACGATGCC
  62
   82 GlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLysGly
  LeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeuCys 181
   LeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGln 141
  IleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeu 217
  ThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGly 201
  AsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAla 161
   PheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeu 81
   CITY: Rockville
STATE: MD
   CTGCTGATCAAGTGCCGTCGCGCCTTG----AAGCAGACCGGCCTG-----AAG
  CAG-----ACCCGCTGCGACATCGCCCTGGCGTTCCAGACCGCGGTGGTCGAGACC
  SerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHis
   ProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCys 41
NAME: Michelle S. Marks
  COUNTRY: USA
   ACCGACAATGGCGCGATGATCGCCTACGCCGGCTGCCAGCGCCTGCTCGCCGGC--
   CTGGAAAAGATGCTCGGCGAAATGAAGGGGCAGGTGTTCTACGCCCGCGCCCGCGCTTCTGC
  AAC-----CTGGTGATCGCCGGCGGTGTCAGCGCCAACCAGGCGCTGCGCAGCGGC 1026
  Genome, Fragments
  930
  822
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   975
   879
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  RESULT 11
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   US-10-649-273-2_COPY_176_414 (1-239) x US-09-557-884-1 (1-1830121)
  Percent Similarity:
Best Local Similarity:
  Query Match:
   Alignment Scores:
  US-09-557-884-1
  Sequence 1, Application US/09643990A Patent No. 6528289 GENERAL INFORMATION:
   INFORMATION FOR SEQ ID NO: 1:
   . No.:
   552572 AAAACATTTGCCGCAAATACAGTTAATCAAGCAATTAAAAACGAGGGCGAACTGATAGAG 552513
   552632 TICACATTTCCACGTCCAATGACAGATCGTGCAGGCCTTGATTTTAGTTTTTCTGGTTTA 552573
  552791 TTAGTGCGTGTCGATGGTGTAGGAAATATGAAGTGATAGGAGAATCTATTGATGATGCT 552732
  552371 GAAACGCTTGCGCACTTAATGCAAAATTTAGGTGGCGAAGTGTTTTATCCTCAACCTCAA 552312
  552467
  552731 GCTGGCGAAGCCTTTGATAAAACAGCAAAATTACTTGGACTA---GATTATCCA-----
                 APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
   TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ
  SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base
TYPE: nucleic acid
STRANDEDNESS: double
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   100 LysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAla 119
  82
   62
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  22
   TTTTGTACAGATAATGGTGCGATGATTGCTTACACAGGTTTTTTTACGTTTAAAAACAAGGT
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   GAAACAGGCTATAAACGTTTAGTGATTGCGGGAGGGGGTGAGCGCAAATAAAAAACTCCGA
   ProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArg
  GATACTCTTGCC----
   CysHisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeu 139
   CAA-----ACTAAAGCAGATATTGCTTATGCTTTCCAAGATGCCGTGGTG 552468
   GlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGly-----IleGlu
   ProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCys 41
   LeuAlaLeuValGlnGlyValSerAspPheLeuLeuGlyLysSerLeuAspIleAla
  ArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProArg 179
   PheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeu
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REFERENCE/DOCKET NUMBER: PB
   TELEFAX: 301-309-8439
Hamilton O. Smith
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224.00
47.50%
33.50%
18.06%
   GGTGGCGCGCACTTTCTCGTTTAGCGGAAAAAGGTACGCCAAATCGT 552633
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  6 2 8 3
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   1830121
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Query Match:
DB:
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  US-10-649-273-2_COPY_176_414 (1-239) x US-09-643-990A-1 (1-1830121)
  Best Local Similarity:
   Percent Similarity:
   US-09-643-990A-1
   INFORMATION FOR SEQ ID NO: 1:
  552731
  APPLICATION NUMBER: 08/426,787
FILLING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
  ZIP: 20850
COMPUTER REALABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskett
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
  J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
  SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
   SEQUENCE DESCRIPTION: SEQ
   NUMBER OF SEQUENCES: 1
   42
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COUNTRY: U
LysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAla 119
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  TCACATTTCCACGTCCAATGACAGATCGTGCAGGCCTTGATTTTAGTTTTTCTGGTTTA
  GCTGGCGAAGCCTTTGATAAAACAGCAAAATTACTTGGACTA---GATTATCCA-----
  ProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCys 41
   TTAGTGCGTGTCGATGGTGTAGGAAAATATGAAGTGATAGGAGAATCTATTGATGATGCT
   GlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGly-----IleGlu
  SerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHis
   TYPE: nucleic acid
STRANDEDNESS: double
   PheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeu
  TOPOLOGY: linear
  TELEPHONE: 301-610-5790
  STREET: 9410 Key West Avenue
  TELEFAX: 310-309-8439
   ITY: Rockville,
   USA
   7.8e-15
224.00
47.50%
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18.06%
   Thereof, and Uses Thereof
  GGCGCGCACTTTCTCGTTTAGCGGAAAAAGGTACGCCAAATCGT 552633
   inch diskette
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   NO:
   Length:
Matches:
  Mismatches:
Indels:
   Conservative:
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  US-10-649-273-2_COPY_176_414 (1-239) x US-09-902-540-6612 (1-996)
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  US-09-902-540-6612
   Percent Similarity:
   Sequence 6612, Application Patent No. 6833447
  SEQ ID NO 6612
  GENERAL INFORMATION:
  APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
   NUMBER OF SEQ ID NOS: 16825
   PRIOR APPLICATION NUMBER: 60/217,883 PRIOR FILING DATE: 2000-07-10
   APPLICANT: Goldman,
  LENGTH: 996
TYPE: DNA
ORGANISM: Myxococcus xanthus
  552512 CAA------ACTAAAGCAGATATTGCTTATGCTTTCCAAGATGCGTGGTG 552468
   552371 GAAACGCTTGCGCACTTAATGCAAAATTTAGGTGGCGAAGTGTTTTATCCTCAACCTCAA 552312
  552431 GAAACAGGCTATAAACGTTTÄGTGATTGCGGGÄGGGGTGAGCGCAAATAAAAAAACTCCGA
  552467 GATACTCTTGCC---
101 GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys 120
  493
   81
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LENGTH: 2582
TYPE: DNA
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   GENERAL INFORMATION:
   APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Myxococcus xanthus Genome Sequences and FILE REFERENCE: 38-10(15849)B
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TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
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CURRENT FILING DATE: 2000-04-05
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PRIOR TILING DATE: 1999-04-09
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIBS

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## ALIGNMENTS

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US-10-120-988-177

(Sequence 177, Application US/10120988

Publication No. US20030219745A1

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APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Mang, Dunrui
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030219745A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802CON
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CURRENT PILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 09/774,528
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PRIOR PILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt_FL genes Version 2.0
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1240.00
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Mismatches:
Indels:
Gaps:
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CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
LENGTH: 1526
TYPE: DNA
ORGANISM: homo sapiens
US-10-067-443-23
   Percent Similarity:
Best Local Similarity:
Query Match:
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  US-10-649-273-2_COPY_176_414 (1-239)
   Pred. No.:
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   Mismatches:
Indels:
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                239
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APPLICANT: BRISTOL-Hyers Squibb Company
TITLE OF INVENTION: POLYNCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 CNT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/264,43
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/67,443
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOPTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 1526
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Query Match:
  ; TYPE: DNA; ORGANISM: homo sapiens US-10-649-273-23
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  Percent Similarity:
  Score:
  Pred. No.:
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   Sequence 23, Application US/10649273 Publication No. US20040043407A1 GENERAL INFORMATION:
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  Indels:
  Mismatches:
  Matches:
Conservative:
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CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR PILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
   Sequence 23, Application US/10651722
Publication No. US20040048302A1
GENERAL INFORMATION:
   SOFTWARE: PatentIn version 3.2 SEQ ID NO 23
   APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
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445
                               121
  385
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Matches:
Conservative:
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Indels:
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Sequence 1, Application US/10067443

Publication No. US20030082782A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED I

TITLE OF INVENTION: SPINAL CORD, MP-1

FILE REFERENCE: D0073 NP

CURRENT APPLICATION NUMBER: US/10/067,443

CURRENT FILING DATE: 2002-02-05

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: US 60/282,814

PRIOR FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin version 3.0

SEQ ID NO 1

LENGTH: 2197
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100.00%
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Conservative:
   Mismatches:
Indels:
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Sequence 1. Application US/10649273

; Publication No. US20040043407A1

; GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITILE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1

; FILE REFERENCE: D0073 CNT
; CURRENT APPLICATION NUMBER: US/10/649,273

; CURRENT FILING DATE: 2003-08-27

; PRIOR APPLICATION NUMBER: US 60/266,518

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; PRIOR APPLICATION NUMBER: US 60/282,814

; PRIOR FILING DATE: 2001-02-05

; PRIOR FILING DATE: 2001-04-10

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: Patentin version 3.2
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Query Match:
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   Score:
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   US-10-649-273-1
  SEQ ID NO 1
   TYPE: DNA
ORGANISM: Homo :
FEATURE:
  NAME/KEY: CDS
LOCATION: (23)
  LENGTH: 2197
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  LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuGlyLysSerLeuAspIle
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17
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   Length: Matches:
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CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 1
LENGTH: 2197
TYPE: DAT
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, NAME/KEY: CDS

; LOCATION: (231)..(1472)

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  Sequence 1, Application US/10651722 Publication No. US20040048302A1 GENERAL INFORMATION:
  APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
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   US-10-649-273-2_COPY_176_414 (1-239) x US-10-651-722-1 (1-2197)
  Sequence 21, Application US/100 Publication No. US20030082782A1 GENERAL INFORMATION:
 SEQ ID
           APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: DO073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
NUMBER OF SEQ ID NOS: 71
NUMBER: Patentin version 3.0
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  100.00%
100.00%
100.00%
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US-10-067-443-21
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90.15%
97.86%
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  US-10-649-273-2_COPY_176_414 (1-239) x US-10-649-273-21 (1-1387)
  DB:
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  CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
   Sequence 21, Application US/10649273

Publication No. US20040043407A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE,

FILE REFERENCE: D0073 CNT
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1213.50
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90.15%
97.86%
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Matches:
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   US-10-649-273-2_COPY_176_414 (1-239)
  Percent Similarity:
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   Sequence 21, Applica Publication No. US20 GENERAL INFORMATION:
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  APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REPERENCE: DO073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/667,443
PRIOR PILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2002-04-10
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Mismatches:
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Sequence 6, Application US/10012140
Publication No. US20030009017A1
GENERAL INFORMATION:
APPLICANT: Leiby, Kevin R.
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 381552004900
CURRENT APPLICATION NUMBER: US/10/012,140
CURRENT APPLICATION NUMBER: 60/246,768
PRIOR APPLICATION NUMBER: 60/246,768
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR FILING DATE: 2000-11-15
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  Pred. No.:
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CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 60/246,768
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR PILING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-08
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PRIOR FILING DATE: 2000-11-15
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  APPLICANT: Leiby, Kevin R.
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 381552004900
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Sequence 400, Application US/10094749
publication No. US20030219741A1
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APPLICANT: ISCAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

WAKAMATSU, AI SATO, HIROYUKI

ISONO,

SHIZUKO TO, JUN-ICHI YUUKO

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APPLICANT: NASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
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   LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
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YOSHIKAWA, TSUTOMU
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  APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Clotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of So
TITLE OF INVENTION: Methods for Screening for
TITLE REFERENCE: 0582 0193.NUSO
FILE REFERENCE: 0582 0193.NUSO
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR PILING DATE: 2002-11-26
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   US-10-649-273-2_COPY_176_414 (1-239) x US-10-723-860-7447 (1-2890)
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  1 LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle
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|         |                                                                          | GCCATAGAACATTTGGCCAAACAAGGAAATTTGATTTTGACATCAAACCTCCCTTG | 49 AlaileGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAsplleLysProProLeu 68 |                                                             | 29      | 649-273-2 COPY 176 414 (1-239) x US-10-067-443-                          | 58.47% Indels: | t Similarity: 32.86%                                                     | 8.93e-83 Length:<br>725.00 Matches: | Alignment Scores:                                                         | ORGANISM: homo sapiens | TYPE: DNA                                                                 | SOFTWARE: PatentIn version 3.0 | PRIOR FILING DATE: 2001-04-10                                            | IOR APPLICATION NUMBER: US 60/282.814 |                                                               | FILE REFERENCE: D0073 NP CURRENT APPLICATION NUMBER: US/10/067.443 | TITLE OF INVENTION: POLYNUCLECTION ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED I | ERAL INFORMATION:<br>PLICANT: Bristol-Myers Squibb Company | Sequence 20, Application US/10067443 Publication No. US20030082782A1     | RESULT 15<br>US-10-067-443-20 | 2114 ATATCAAAAGAAGTTGGAGAAGCTTCCATAAAAAGTACCACAATTAAAAATGGAGATA 2170     | 221 IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 239 | 2093                                                                     | 201 GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp 220 | 181 CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu 200<br>                               | 2006 GCTCTGGAAATTTTAACAAACGCAACACAGTGCACTTTGTTGTTGTCCTCCTCCCAGACTA 2065  | 161 AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProArgLeu 180    | 1946 CAAAATAATGCAGTACTGGTTGCATCTGGTGGTGTCGCAAGTAACTTCTGTATCCGCAGA 2005   | 141 GlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg 160 | 121 HisteuValLysArgThrHisArgAlalIeLeuPheCysLysGlnArgAspLeuLeuPro 140 |   |
|---------|--------------------------------------------------------------------------|----------------------------------------------------------|--------------------------------------------------------------------|-------------------------------------------------------------|---------|--------------------------------------------------------------------------|----------------|--------------------------------------------------------------------------|-------------------------------------|---------------------------------------------------------------------------|------------------------|---------------------------------------------------------------------------|--------------------------------|--------------------------------------------------------------------------|---------------------------------------|---------------------------------------------------------------|--------------------------------------------------------------------|---------------------------------------------------------------------------------------|------------------------------------------------------------|--------------------------------------------------------------------------|-------------------------------|--------------------------------------------------------------------------|-------------------------------------------------------------------|--------------------------------------------------------------------------|----------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------|----------------------------------------------------------------------|--------------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|---|
| 8       | рb                                                                       | \$ E                                                     | ş 2                                                                | д                                                           | Q       | Ъ                                                                        | δ              | Ъ                                                                        | Ą                                   | Ъ                                                                         | Q<br>Q                 | ДЪ                                                                        | Ş                              | ДЪ                                                                       | 8                                     | рь                                                            | Ŋ                                                                  | ф                                                                                     | δ                                                          | ф                                                                        | · Q9                          | дb                                                                       | δ                                                                 | ď۵                                                                       | Q                                                                    | gy<br>Qy                                                                                               | da                                                                       | 8                                                                    | 망                                                                        | Q                                                                    | B 8                                                                  | 1 |
| 146 146 | 13040 TTTTTCTTTCCAAATTTTTATTACATAGATATGTCATCTGCCCATTACCCATCTCAAAAT 13099 | 146 146                                                  | 146                                                                | AGGGTCTAAAATAGTGTACTATGATTGAAATTATATTAAATAATATTTAGATGAAAGGT | 146 146 | 12860 ATATCAAAGAATAATTTTTTCAGAGTTATGTAGTAAAATGCACAAAATAATAAAAATTTC 12919 | 146 146        | 12800 TATAAACTAAAGTGGGAAAATGTTTAAATGGTAGTAATTCATAGATGGAATTTTACATGG 12859 | 146 146                             | 12740 CTTAAAAGCCTTGACAAACATCCTGTTTAACTGTATCTTAAACTTTTATTCATTTAAAAAT 12799 | 146 146                | 12680 AATGTTGATAAAGTTCTGATAATCCACTATATTGTACCAGCCAAAATCCCCTTTAATTGTG 12739 | 146 146                        | 12620 TTTTTTAATAAGCCAGTCAAATTTAGCAGTGGGAGGTGGTATTCCAACTTTCGTGACACT 12679 | 146 146                               | 12560 ATTTTTAGAAAAATAGGTGGATTTCCTTCATCCTTTGATGAAATCCCTTTGTTTG | 146 146                                                            | 12500 CTTGTTGGATTTAAAAGAGGGCTTACAATAAAGAAAGTAAATGCAGTAACTGCTATCACT 12559              | 146 146                                                    | 12440 TGGTAGCTTTATGGGACAGCTGTATAGCTTCTATGGCACATAAGTCTAATTTTGCATCTT 12499 | 146 146                       | 12380 CCCTGACAGTATGAAATTATGCAGGATAGGAAAGACTAACAGCCATTTCTTGTACTAGTT 12439 | 146 146                                                           | 12320 TTTTTTCCCAAGACCTTGACCTTGTGTTTAGGATGAACAGATCTTTATGCCTTATGCTAG 12379 | 146 146                                                              | 143 nAlaValLeu 146            12260 TGCAGTACTGGTAAGTTTTATCTCATTTTATAGTAATAGTTACACTTTGCAATATGTTAC 12319 | 12200 GAAAAGAACACATCGGGCTATTCTGTTATGTAAGCAGAGACACTTGTTACCTCAAAATAA 12259 | 123 llysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAs 143 | 12140 CCTGTCTTCAGCAGCAGACATTGCTGCCACAGTACAGCACACAATGGCATGTCATCTTGT 12199 | 103 eLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuVa 123 | 97                                                                   |   |

|       | 13520 ĠĊŢĀŢĠĀĀĊĊĀĀĀĠ 13533                                                | 13520 | DЪ       |
|-------|---------------------------------------------------------------------------|-------|----------|
|       | rgTyrGluProLys 214                                                        | 210   | Ş        |
| 13519 | 13460 GGAATGGTATTGAAAGACTACGTGCTGGCTTGGGCATTTTACATGACATAGAAGGCATCC 13519  | 13460 | 40       |
| 210   | AsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleA                | 191   | 8        |
| 13459 | 13400 ACTAAGCCTTCCTTCCTTCAGATCTTGGAGCTATTGATTTATTT                        | 13400 | da<br>qa |
| 190   |                                                                           | 190   | γQ       |
| 13399 | 13340 AGCCACAGGATATACGTGCTTCACTCATAACTATGTAAATATTAATTGCCATTTTATCAT 13399  | 13340 | Db       |
| 190   |                                                                           | 190   | γŞ       |
| 13339 | CACTTTGTTGTGTCCTCCTCCAGACTATGCACTGATAATGGCATTATGATTGCATGGTA 13339         | 13280 | ם        |
| 190   |                                                                           | 171   | β        |
| 13279 | TGTCGCAAGTAACTTCTATATCCGCAGAGCTCTGGAAATTTTTAACAAACGCAACACAGTG             | 13220 | фa       |
| 171   | yValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCy              | 151   | છ        |
| 13219 | 13160 TCATATCCATATATGATAGTTATTTTGGTTTTCTCAATTCCTTCAGGTTGCATCTGGTGG 13219  | 13160 | фq       |
| 151   | ValAlaSerGlyGl                                                            | 147   | δδ       |
| 13159 | 13100. GGGATAGTTTATTATTGTTTAATGCTGATATTTTTCTCCAGGTTTAATTAGCAGCTTGGT 13159 | 13100 | מַ ַ ם   |

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| 1 LL2 221 LL1 221 LL1 61 HPI 276 SVI 121 HL3 126 HL1 1326 HL1 181 CTI 183 CTI                                                                             | Eamily: Eamily: Match Mocal S                                    | A;Reference number: A84 A;Accession: E84888 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-463 <sto> A;Cross-references: GB: C;Genetics: C;Genetics: A;Gene: At245270</sto> | on: 884 ; Kaul, H.; Mof Nierma 2, 761- Sequenc                                            | 2-B                                                                          | 193<br>192<br>192<br>188.5<br>186.5<br>186.5<br>186.5<br>186.5<br>174.5<br>179                                                                                                                                                                                                                                                                                                                                                                         |
| LLALVQGVSDFILLGK                                                                                                                                          | esialoglycopr<br>26.<br>Conservative                             | ar: A84420;<br>388<br>lnary<br>DNA<br>3 <sto><br/>5: GB:AE00</sto>                                                                                                                    | 888<br>S.; Rouns<br>fat, K.S.<br>n, W.C.; V<br>768, 1999<br>e and ana.                    | glycopro<br>lopsis t                                                         | 11111111111111111111111111111111111111                                                                                                                                                                                                                                                                                                                                                                                                                 |
|                                                                                                                                                           | sialoglycoprotein 26.3%; ; larity 33.6%; ; Conservative 34       | A84420; MUID Y TO> GB:AE002093;                                                                                                                                                       | Rounsley, S.D<br>K.S.; Cronin,<br>C.; White, O.<br>1999                                   | otein er<br>thaliana                                                         | 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                                |
| SLDIAPGI TVDDAIGE TVDDAIGE SPTGLQHV SPTGLQHV SYAGLKTC CLLPQNNI CLLPQNNI CLLPQNNI RAGLGILH RVG                                                             | cein endop<br>h; Score<br>h; Pred.<br>34; Mis                    | MUID:20083487;<br>093; NID:g2583                                                                                                                                                      | Ch ', ' D ', '                                                                            | ALIGNM  oprotein endopeptidase is thaliana (mouse-ear #sequence_revision 02- | 2 \$75548<br>2 AF1820<br>2 CH70195<br>2 CH70195<br>2 CH70134<br>2 AC1334<br>2 H70737<br>2 BH70737<br>2 BH70737<br>2 DB3718<br>2 DB3718<br>2 DA71545<br>2 DA71545<br>2 DA71545<br>2 DA61471<br>2 CA64436<br>2 E84936<br>2 E84936<br>2 E84936<br>2 T35581                                                                                                                                                                                                |
| LIALVQGVSDFLLIGKSLDIAPGIMLDKVARRI                                                                                                                         | endopeptidase<br>Score 326; DB<br>Pred. No. 4.3e<br>; Mismatches | ₽                                                                                                                                                                                     | 8 5                                                                                       | - 19 D                                                                       | ## ## ## ## ## ## ## ## ## ## ## ## ##                                                                                                                                                                                                                                                                                                                                                                                                                 |
| LLALVGVSDFLLLGKSLDIA PGDMLDKVARRLSLIKHP                                                                                                                   | dase<br>DB 2;<br>4.3e-22;<br>hes 84;                             | _                                                                                                                                                                                     | o ~ <b>3</b> ~                                                                            | porte                                                                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| ECST KGQI RALB LRLN PEDY                                                                                                                                  | Length 463; Indels                                               |                                                                                                                                                                                       |                                                                                           | ext -                                                                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| MSGGKAIEHLAKCORRF<br>                  <br>RSGGPAVEELALEGDAK<br>LSRAGGPAVELATEGDAK<br>LSRAGIAATPORTMAC<br>                                                | 463;<br>8 44;                                                    |                                                                                                                                                                                       | ; Tov<br>.E.;<br>L.; F                                                                    | סי                                                                           | sialoglycoprote<br>sialoglycoprote<br>O-sialoglycoprote<br>O-sialoglycopro<br>glycoprotein en<br>grobable o-sial<br>grobable o-sial<br>grobable o-sial<br>o-sialoglycopro<br>o-sialoglycopro<br>o-sialoglycopro<br>o-sialoglycopro<br>o-sialoglycopro<br>o-sialoglycopro<br>o-sialoglycopro<br>probable O-sial                                                                                                                                         |
| AIEHLAKÇÜNRF<br> :    : <br>AVEELALEGDAK<br>DIAATVOHTMAC<br>    : <br>DIAASPORVAVL<br>DIAASPORVAVL<br> :     <br>KNILKIVCPPPSL<br>PKCPLGVDISKE<br> :   :: | Gaps                                                             | 2                                                                                                                                                                                     | · 3 D                                                                                     | sis thaliana<br>02-Jun-2003                                                  | sialoglycoproteina<br>sialoglycoproteina<br>cialoglycoproteina<br>O-sialoglycoprotein<br>O-sialoglycoprotein<br>glycoprotein endop<br>grobable o-sialogl<br>glycoprotein endop<br>probable o-sialogl<br>o-sialoglycoprotei<br>o-sialoglycoprotei<br>o-sialoglycoprotei<br>o-sialoglycoprotei<br>o-sialoglycoprotei<br>o-sialoglycoprotei<br>o-sialoglycoprotei<br>o-sialoglycoprotei<br>o-sialoglycoprotei<br>o-sialoglycoprotei<br>o-sialoglycoprotei |
| 275<br>120<br>325<br>382<br>382<br>224                                                                                                                    | 5;                                                               | ω<br><b>6</b>                                                                                                                                                                         | uji<br>; T                                                                                | <u> </u>                                                                     | ggl                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|                                                                                                                                                           |                                                                  |                                                                                                                                                                                       | i, C.Y.; Nallon, L.c.<br>Venter, J.                                                       |                                                                              | ,i                                                                                                                                                                                                                                                                                                                                                                                                                                                     |

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C;Accession: AB2902
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, R;Wood, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, F.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Go.
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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
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   A; Map position: circular chromosome C; Superfamily: O-sialoglycoprotein endopeptidase
   A;Status: preliminary A;Molecule type: DNA
   A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58 A;Reference number: AB2577; MUID:21608550; PMID:11743193 A;Accession: AB2902
  A; Status: preliminary
   A;Cross-references: GB:AB008688; PIDN:AAL43632.1; PID:g17741154; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
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   A;Residues:
   Query Match
Best Local S
Matches 73
  Matches
  Superfamily: O-sialoglycoprotein endopeptidase
   Query Match
   Genetics:
  Local
  118 MACHLVKRTHRAILFCKQRDLLFQNNA--VLVASGGVASNFYIRRALBILTNATQCTLLC 175
  149 LVLVRGVGEYERWGTTIDDALGEAFDKTAKLLGL-PYP-----GGPAVENAAAKGDPDR
  251 VSRTLKDRIGRGLARFKVE--FPHINGEPALVVAGGVAANQEIRQTLQALCDTHGFRFVA
  202 FPLPRPMVGEARLDFSFSGLKTAVRQAATAIAPLSEQD-----IADICASFQKA
   62
  62
   2 LALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFH
   2 LALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFH
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Similarity 31.9%; Pred. No. 1.1e-14;
  1-365 <KUR>
  Similarity
  PPPRLCTDNGIMIAWNGIERLRAGIGILHDIEGIRYEPKCPLGVDISKE 224
     FPLPRPMVGEARLDFSFSGLKTAVRQAATAIAPLSEQD--
   FDIKPPLHHAKNCDFSFTGL----QHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHT 117
   LVLVRGVGEYERWGTTIDDALGEAFDKTAKLLGL-PYP-----GGPAVENAAKGDPDR 202
   FDIKPPLHHAKNCDFSFTGL----QHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHT 117
  PPHRLCTDNAAMIAWAGLERMAEG----RQADALEVAPRSRWPLDGSAE 353
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   Conservative
   19.7%; Score 244; DB 2;
31.9%; Pred. No. 1.1e-14;
rative 34; Mismatches 92
   34; Mismatches
   92;
  Length 365;
   Length 366;
  Indels
   Indels
     -IADICASFQKA 251
  30;
   30;
  Perry, M.; Gordon-Kamm,
  Gaps
  Gaps
   308
  61
  201
  250
  , Y.; Woo,
M.; McClel
   probable o-sialoglycoprotein endopeptidase (gcp) RP037 - Rickettsia prowazekii C;Species: Rickettsia prowazekii C;Species: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004 C;Accession: E71711 R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998 A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893 A;Accession: E71711
  RESULT 5
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A;Gene: gcp; RP037
C;Superfamily: O-sialoglycoprotein endopeptidase
  A; Experimental source: C; Genetics:
  A;Cross-references: UNIPROT:Q9ZEA8; GB:AJ235270; A;Experimental source: strain Madrid E
  A; Molecule type: DNA
A; Residues: 1-387 < AND >
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   ð
  A; Status: preliminary; nucleic acid sequence not shown; translation not
  Matches
  Query Match
  304
   176
  310
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   62
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi A;Reference number: AD3252; PMID:11756688
A;Accession: AB3274
   A;Map position: I
C;Superfamily: O-sialoglycoprotein endopeptidase
C;Keywords: hydrolase; metalloproteinase
  O-sialoglycoprotein endopeptidase (BC 3.4.24.57) [imported] - Brucella melitensis (strair C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
  A;Cross-references: GB:AB008917; PIDN:AAL51357.1; PID:g17982056; GSPDB:GN00190
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  198 FALPRPLKGEARLDFSFSGLKTAVRQTATELVPLTDQ--
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   118 MACHLVKRTHRAILFCKQRDLLFQNNA--VLVASGGVASNFYIRRALEILTNATQCTLLC
  69;
  2 LALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFH
  AVADTLSDRVGRSLERFKTE--FPDCATPSLVVAGGVAANKTLRAALENLCTRHGFAFIA 303
   TMACHLVKRTHRAILFCKQRDLLPQ-NNAVLVASGGVASNFYIRRALBILTNATQCTLLC 175
  FDIKPPLHHAKNCDFSFTGL----QHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQH 116
  PPHRICTDNAAMIAWAGLERMAEG----RQADALEVAPRSRWPLDGSAE
   VSRTLKDRIGRGLARFKVE--FPHINGEPALVVAGGVAANQEIRQTLQALCDTHGFRFVA 309
PPLNLCTDNAAMIAWAGAER 323
  PPPRLCTDNGIMIAWNGIER 195
  PPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKE 224
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  19.5%; Score 241.5; DB 2; 34.5%; Pred. No. 1.9e-14; ative 27; Mismatches 77;
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  -GGPAVERMALQGDQKR 197
  ----DVTDICASFQA
   27;
  Gaps
  13
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GB:AJ235269; NID:g3860572; PIDN:CAA14508

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C;Accession: HB3572
R;Stover, C.K.; Pham, X.Q.; Erwin, adman, S.; Yuan, Y.; Brody, L.L.; (...; Lory, S.; Olson, M.V.
   O-sialoglycoprotein endopeptidase PA0580 [imported] - Pseudomonas aeruginos
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
   A;Cross-references: GB:AE005673; NID:g13421168; PIDN:AAK22058.1; GSPDB:GN00148 C;Genetics:
"A;Gene: CC0071
C;Superfamily: O-sialoglycoprotein endopeptidase
  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-367 <STO>
  R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koln, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87257
  peptidase M22 family protein [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001 C;Accession: F87257
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Matches 70; Conserv
  310
   260
  125
  209
   143
   124
   145
   156 VSGVGACKRLGTTIDDAAGEAFDKIAKSLGL-PYP-----GGPALEKLAVGGDPTRYAL
  65 KPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVK 124
  σ
  73;
   v
  Similarity
   GIMIAWNGIERLRAGIGILHDIEGIRYEPKCPL 217
   VQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDI
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  AAMIALAGAERI -- ALGIFDDLDAIA - RPRWPL 347
   RVDRAMKLYK--DSHDPEDLRFVVAGGVAANGAVRAALLADCEKNGFSFAAPPLAYCTON
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  PRALLGRKDCDFSFSGLKTAAARIAETLTTDD-----ARRDLAAGVQAAIARQLSE
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   KRTHRAILFCKQ-----
  KPPLHHAKNCDFSFTGLQHVTDKIIMK-KEKEEGIEKGQILSSAADIAATVQHTMACHLV 123
   VLGLGKYKILGTTIDDAVGETFDKVAKMLNL----SFPGGPEIEKRAKLGNPHKYKF 197
   VQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDI
  --- NAVLVASGGVASNEYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIER 195
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34.3%; Pred. No. 4.6e-14;
vative 29; Mismatches 90
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                                A.L.; Mizoguchi, S.D.; Warrener, Coulter, S.N.; Folger, K.R.; Kas,
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  21;
  <del>,</del>09
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  Gaps
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Larbig,
   208
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   142
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   (strain
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A;Gene: gcp
C;Superfamily: O-sialoglycoprotein endopeptidase
C;Keywords: hydrolase; metalloproteinase
   R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.B.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: E97707
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A;Residues: 1-344 <KUR>
A;Cross-references: GB:
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  A;Cross-references: GB:AE004494; GB:AE004091; NID:g9946446; A;Experimental source: strain PAO1
   A;Reference number: A82950;
A;Accession: H83572
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   Genetics:
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308
  183
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  145 VLGLGKYKILGSTIDDAVGBAFDKVAKWLNL-----APPGGPBIBKRAKLGDPHKYKF 197
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   251
   122
  195
  142 LVRVDGIGRYQLLGESVDDAAGEAFDKTAKLIGL-GYP-----GGPEIARLAERGTPGR 194
   65
   62
   64;
  ហ
   N
   Similarity
DNAAMIAYAGLER
   DNGIMIAWNGIER
  KRTHRAILFCKQ-RDLLPQNNAVLVASGGVASNFYIRRALBILTNATQCTLLCPPPRLCT 182
  KPPLHHAKNCDPSPTGLQHVTDKIIMK-KEKEEGIEKGQILSSAADIAATVQHTMACHLV 123
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   FVFPRPMTDRPGLDFSFSGLKTFTLN-TWQRCVEAGDDSEQ-
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  TDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPL 217
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  18.6%; Score 231; DB 2; ilarity 33.8%; Pred. No. 1.6e-13; Conservative 34; Mismatches 87
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   GB:AE006914;
  18.6%; Score 230.5; DB 2
33.2%; Pred. No. 1.9e-13;
320
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   Length
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   Length
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   19;
  22;
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  opportunistic
  249
  307
   302
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   G59388

G-sialoglycoprotein endopeptidase homolog - Archaeoglobus fulgidus
C-species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
C;Accession: G69388
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: G69388
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A; Residues: 1-323 < KLE>
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C;Keywords: hydrolase; metalloproteinase
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C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: H64074
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
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   A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
  ; Gocayne, J.D.; Scott, J.; Shirley, D.M.; Brandon, R.C.; Fine, L.D.; Science 269, 496-512, 1995
   A;Status: nucleic acid sequence not shown; translation not shown
  A; Accession: H64074
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  ;Superfamily: O-sialoglycoprotein endopeptidase
  Cross-references: GB:AE001027; GB:AE000782; NID:g2689350; PIDN:AAB90129.1; PID:g26494
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   302
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   FLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHH 70
   FCTDNGAMIAYTGFLRLKQG
  LCTDNGIMIAWNGIERLRAG 199
  CHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPR 179
  FTFPRPMTDRAGLDFSFSGLKTFAANTVNQAIKNEGELIEQ----TKADIAYAFQDAVV
  FDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEG--IEKGQILSSAADIAATVQHTMA 119
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  17.9%;
  30;
   Score 221.5; DB 2
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   66;
   83;
   Length 342;
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                    A;Residues: 1-335 <AQF>
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th, T.; Connertum, 2., 2., 8.; Moule, S.; O'Gaora, P.
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Title: Complete genome sequence of a multiple drug resistant
A;Title: AB0502; MUID:21534947; PMID:11677608
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c;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change
C;Accession: G70369
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox
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G70369
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C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change
C;Accession: AG0892
   RESULT 11
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  A;Title: The complete genome of the hyperthermophilic bacterium A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: G70369
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A; Residues: 1-337 < PAR>
   R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Clth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.;
A; Molecule
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  NGIERLRAG 199
  LFCKORDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAW 190
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   FDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACH 121
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                       sequence
   Mismatches
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  331
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  Length 337;
   Indels
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Salmonella enterica
  enterica serovar
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  09-Jul-2004
  18-Nov-2002
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  A.L.; Graham,
                          not
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  61
  Stevens, K.;
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  290
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F75029
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R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
   A;Cross-references: UNIPROT:O66986; GB:AE000708; NID:g2983356; PIDN:AAC06951.1; PID:g298
A;Experimental source: strain VF5
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o-sialoglycoprotein endopeptidase C; Species: Pyrococcus abyssi
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   A;Accession: AI0079
A;Status: preliminary
  A; Title: Genome sequence of Yersinia pestis, the causative agent of plague A; Reference number: ABO001; MUID:21470413; PMID:11586360
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Fgasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
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  26;
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GenCore version 5.1.6 (c) 1993 - 2005 Compus

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Maximum DB
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## ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL ACCESSION VERSION KEYWORDS SOURCE RESULT 1 BQ423651 LOCUS DEFINITION **FEATURES** COMMENT ORGANISM source Contact: KODELL COLLEGE OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE METERS OF THE BQ423651 BQ423651 AGENCOURT 7790948 NIH\_MGC\_72 H
5', mRNA sequence.
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Unpublished (1999)
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1118.00
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  Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K. Expressed sequence tag analysis of human retina for the NEIBank Project: Retbindin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts Mol. Vis. 8 (4), 196-204 (2002)
  Email: graeme@helix.nih.gov
Plate: 03 row: d column: 11
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  Tel: 301 402 3452 Fax: 301 496 0078
  National Eye Institute 6/331, NIH, Bethesda, N
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Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the SuperScript Plasmid System full
details of which are contained in the manufacturer's
Instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
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was performed on the unamplified library at the NIH
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   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected subtraction prepare full-length cDNA libraries for rapid discovery of new captures.
   Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
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26 (bases 1 to 2284)

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28 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiramoto, K., Hiramoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Hiramoka, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku, Akahira, S., Muramatsu, M., and Hayashizaki, Y.
   Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GS RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yok Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
   prepare mouse tissues.
Please visit our web site for further details.
   cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in R.
Genomic Sciences Center and Genome Science Laboratory in RIKEN
   Group Phase I & II Team.
Analysis of the mouse transcriptome based on of 60,770 full-length CDNAs
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URL:http://fantom.gsc.riken.jp/.
   Division of Experimental Animal Research in Riken contributed
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Functional annotation of a full-length mouse
  The RIKEN Genome Exploration Research Group Phase
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  RIKEN Genome
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enriched mouse

cDNA library"

100% length,

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  Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                 Physical and Chemical Research (RIKEN), Laboratory for Gen Exploration Research Group, RIKEN Genomic Sciences Center RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
   Group Phase I & II Team.
Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
   Functional annotation of a Nature 409, 685-690 (2001)
  Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999)
  Nature 420, 563-573
6 (bases 1 to 1622)
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1 LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle 20

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AUTHORS
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 13, 2003 this sequence version replaced gi:30611736.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
  Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
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into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
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Mismatches:
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   COMMENT
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   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 66 Row: e Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312463
This clone has the following problem: frame shifted.

Location/Qualifiers
   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, University of
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
   Submitted (20-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
  http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton,
Madan, Stephanie Rodrigues, Amy Sanchez
  Direct Submission
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  Mark Ketteman, Anura
   1609
183
12
20
24
   Anuradha
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120 1048 988 80 928 60 868 40 808 \$ В S 망 Ś 밁 ð 밁 Ś

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REFERENCE
AUTHORS
TITLE
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 Percent Similarity:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
   Contact: Robert Strausberg, Ph. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.
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insert size 1.8kb. Library constructed by Ling Hong in
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Mismatches:
Indels:
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Contact: Smith TPL
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Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W. A. second set of porcine ESTs from a pooled-tissue normalize.
  _
  Email: smith@email.marc.usda.gov
   USDA, ARS, US Meat Animal PO Box 166, Clay Center, N Tel: 402 762 4366
Fax: 402 762 4390
   library
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   HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
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NE 68933-0166,
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  Contact: Tad S. Sonstegard
Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bdlg. 200 Rm2A BARC-East, Beltsville, M
Tel: 3015048414
Fax: 3015048414
   1 (bases 1 to 637)
Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C. Production of BST from cDNA libraries derived from immunologically activated bovine gut Unpublished (2004)
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   Email: tads@anri.barc.usda.gov
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Conservative:
Mismatches:
Indeis:
Gaps:
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AV602901
                         Shirakawa Institute of Animal Genetics Odakura, Nishigo, Nishi-shirakawa, Pukn Tel: 81-248-25-5641
   Contact: Yoshikazu Sugimoto
   bovine BSTs
Nucleic Acids Res.
   and Sugimoto,Y.

Bstablishment of a high throughput EST sequencing syst poly(A) tail-removed cDNA libraries and determination
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  system
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650 120

Suzuki, H., Aso, H.

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CB852881
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CB852881 490 bp mRNA linear EST 22-AI UI-CF-FNO-afo-b-03-0-UI.sl UI-CF-FNO Homo sapiens cDNA clone UI-CF-FNO-afo-b-03-0-UI 3', mRNA sequence.
   Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing
This clone was obtained from a p
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MEDLINE
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  Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
   Genome Res. 6 (9), 791-806 97044477
  2024 University of Iowa
Tel: 319 356 4866
Fax: 319 356 7171
  Contact: McCray, PB
McCray Lab
  8889548
   discovery
  1 (bases 1 to 490)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approximates approximately.
   Homo sapiens
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   University of Iowa
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Mammalia; Butheria; Primates; Catarrhini; Hominidae;
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AUTHORS
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1 (Dases 1 to 822)
Wittzell,H., Bed'Hom,B., Morin,V., Young,J.R., Whittaker,C.J., Chausse,A.M. and Zoorob,R.
A collection of chicken ESTs from activated immune cells Unpublished (2003)
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I BUI27463.1 GI:25338728

SST.

Gallus gallus (chicken)

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus

1 (bases 1 to 866)

JTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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   Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
  PO Box 88, Manch
Tel: 01612008930
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603114407F1 CSEQCHL20
  Fax: 01612360409
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cloned cDNA libraries from messenger RNA for improved 3'
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6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
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Mismatches:
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JOURNAL
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VERSION
KEYWORDS
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  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
  National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
  Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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mix of male and female animals at 8 wk old. Tissues were
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extraction and purification (Tri-reagent method). cDNA was
primed using oligo-dT primer:
5'-pGACTAGTHCTAGARCGCGAGCGGCCC(T) 25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb
resulted in an average insert size of 2.3 kb. This primary
library is not normalized (normalized primary library is
NIH_MGC 232) and was constructed by Express Genomics
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| Search<br>Job ti                                                         | Ъ                             | Ş                             | В                                                                    | γ                                                                    | Db                                                                   | γŞ                                                                   | В                                                                    | Ş                                                                    | 망                                                                    | Ş                                                                    | Дb                                                                  | β | ρb |
|--------------------------------------------------------------------------|-------------------------------|-------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|---------------------------------------------------------------------|---|----|
| Search completed: February 16, 2005, 21:04:55<br>Job time : 2847.68 secs | 481 CCACCATTAAAAATGACACTT 501 | 233 ProGlnLeuLysMetGluIle 239 | 421 CCAAAATGTCCTCTCGGAATAGACATATCCAGAGAAGTTGCAGAAGCTGCCATAAAAGTA 480 | 213 ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal 232 | 361 ATTGAAAGATTACGTGCTGGCTTGGGCATTTTACATGATGTAGAAGACATCCGATACGAA 420 | 193 IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu 212 | 301 TIGTIGTGTCCCCCTCCGAGACTGTGCACTGACAATGGTATCATGATTGCATGGAATGGA 360 | 173 LeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGly 192 | 241 GCAAGTAACTTGTACATCCGAAGAGCATTGGAAATTGTAGCAAATGCAACACAATGCACT 300 | 153 AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr 172 | 181 TGCCAGCAGAAAATTTGCTATCTCCAGCTAACGCAGTATTAGTTGTGTCTGGAGGTGTT 240 |   |    |

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2005, 10:46:17; Search time 40.5261 Seconds (without alignments) 3019.954 Million cell updates/sec

Title: US-10-649-273-2_COPY_176_414

Perfect score: 1240
Sequence: 1 LLALVQGVSDFLLLGKSLDI.......DISKEVGEASIKVPQLKMEI 239

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries

Database: UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| 30<br>30<br>29                                                | 27<br>28<br>29                                                 | 23<br>25<br>25             | 19<br>20<br>21<br>22                 | 16<br>17<br>18                                                                      | 11<br>12<br>14                                       | 109876                                                                                                                               | льωυμ                                          | Result     |
|---------------------------------------------------------------|----------------------------------------------------------------|----------------------------|--------------------------------------|-------------------------------------------------------------------------------------|------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------|------------|
| 238<br>238<br>237.5                                           | 241.5<br>241.5<br>241.5                                        | 244<br>244                 | 252.5<br>252<br>251<br>246.5         | 257<br>257<br>254<br>253                                                            |                                                      | 983<br>960<br>751<br>747<br>361.5                                                                                                    | 1240<br>1213.5<br>1086<br>1079                 | Ö          |
| 19.2                                                          |                                                                |                            |                                      | 20.7                                                                                |                                                      |                                                                                                                                      | 100.0<br>97.9<br>87.6<br>87.0                  | tch<br>ery |
| 387<br>367                                                    | 6 5 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                      | 387<br>365<br>366          | 346<br>346<br>389                    | 346<br>335<br>362                                                                   | 323<br>480<br>255                                    | 467<br>404<br>404<br>401                                                                                                             | 414<br>414<br>414<br>414<br>414                | Length     |
| 20 11 12                                                      | 0000                                                           | 000                        | N N N N                              | 2022                                                                                |                                                      | N N N N N I                                                                                                                          | งถอกต                                          | BB         |
| C93FUZ<br>GCP_RICPR<br>Q9ABZ9                                 | Q8YJB1<br>Q8FYIS<br>Q9CLJ1                                     | Q68XR3<br>Q8UC47<br>Q7CWJ8 | Q6FCK9<br>Q7W668<br>Q7W134<br>Q6ND54 | Q92LH8<br>Q7VXN4<br>Q73H71<br>Q98EI6                                                | Q960S6<br>Q9VWD6<br>Q97WD6<br>Q677H2                 | Q6AYN7<br>Q6AYN7<br>Q96NH5<br>Q8JFW3<br>Q8JFR7<br>Q7Q918                                                                             | Q96EV9<br>Q9H4B0<br>Q6PEB4<br>Q8BLB6<br>Q8DLB6 | ا ا        |
| Q931u2 cowdria rum<br>Q9zea8 rickettsia<br>Q9abz9 caulobacter | Q8yjb1 brucella me<br>Q8fyi5 brucella su<br>Q9cij1 pasteurella |                            |                                      | Q921n8 rn12001um m<br>Q7vxn4 bordetella<br>Q73h71 wolbachia p<br>Q98ei6 rhizobium 1 | drosophila<br>drosophila<br>arabidopsi<br>hyacinthus | Q6ayn7 rattus norv Q6ayn7 rattus norv Q96nh5 homo sapien Q8jfw3 brachydanio Q8jfr7 brachydanio Q8jfr7 brachydanio Q7q9i8 anopheles q | 001                                            | on         |

| <b>4</b><br>5 | 44          | 43          | 42     | 41          | 40          | 39         | 38         | 37         | 36          | 35          | 34          | ω<br>u     | 32          |
|---------------|-------------|-------------|--------|-------------|-------------|------------|------------|------------|-------------|-------------|-------------|------------|-------------|
| 217           | 219.5       | 221.5       | 223.5  | 224         | 224         | 228.5      | 230.5      | 231        | 231         | 231         | 233.5       | 234.5      | 236.5       |
| 17.5          | 17.7        | 17.9        | 18.0   | 18.1        | 18.1        | 18.4       | 18.6       | 18.6       | 18.6        | 18.6        | 18.8        | 18.9       | 19.1        |
| 341           | 347         | 323         | 344    | 342         | 337         | 353        | 344        | 364        | 341         | 341         | 339         | 344        | 357         |
| N             | N           | N           | N      | <u>بـ</u>   | N           | N          | N          | N          | N           | N           | N           | N          | N           |
| Q8ESI6        | Q8XX97      | 029153      | Q65RP0 | GCP_HAEIN   | Q82XN2      | Q7VQQ9     | Q92JK6     | Q6G1R3     | Q915V7      | Q7NUE3      | Q6LV10      | Q7PAG7     | Q89WW1      |
| Q8esi6        | Q8xx97      | 029153      | Q65rp0 | P43764      | Q82xn2      | Q7vqq9     | Q92jk6     | Q6g1r3     | Q915v7      | Q7nue3      | Q61v10      | Q7pag7     | Q89ww1      |
| oceanobacil   | ralstonia s | archaeoglob |        | haemophilus | nitrosomona | candidatus | rickettsia | bartonella | pseudomonas | chromobacte | photobacter | rickettsia | bradyrhizob |

## ALIGNMENTS

| SEQUENCE PROM N. SEQUENCE PROM N. TISSUE-Muscle; Strausberg R.; Submitted (JUL-2 SEMBL; BC011904; MEROPS; M22.004; GO; GO:0008450; GO; GO:0008270; GO; GO:0006508; InterPro; IPR000 InterPro; IPR000 InterPro; IPR000 InterPro; IPR000 InterPro; IPR000 InterPro; IPR000 InterPro; IPR000 InterPro; IPR000 INTERPNO: SEQUENCE 414 A  | RC TISSUB=Muscle; RX MEDLINE=22388257; PubMed=12477932; DN RA Strausberg R.L., Feingold E.A., Grou Klausner R.D., Colline F.S., Wagner I RA Altschul S.F., Zeeberg B., Buetow K.J. RA Altschul S.F., Jordan H., Moore T., M. Parmer A. Hopkins R.F., Jordan H., Moore T., M. Diatchenko L., Marusina K., Farmer A. RA Brownstein M.J., Usdin T.B., Toshiyul RA Brownstein M.J., Usdin T.B., Toshiyul RA Brownstein M.J., Usdin T.B., Toshiyul RA Raha S.S., Loquellano N.A., Peters G. RA Bosak S.A., McEwan P.J., McKernan K., Ra Richards S., Worley K.C., Hale S., G. RA Pilalon D.K., Muzny D.M., Sodergren RA Whiting M., Madan A., Young A.C., Sha Richards R.W., Touchman J.W., Green RA Blakesley R.W., Touchman J.W., Green RA Krzywinski M.I., Skaliska U., Smailus RA Jones S.J., Marra M.A.; Staliska U., Smailus RA Jones S.J., Marra M.A.; Proc. Natl. Acad. Sci. U.S.A. 99:168; RN [2]                                                                                                                                                                                                                                                                                             | GEV9  096EV9  01-DEC-2001 (TrEMBLz 01-DEC-2001 (TrEMBLz 01-MAR-2004 (TrEMBLz 01-MAR-2004 (TrEMBLz 01-MAR-2004 (TrEMBLz 05GEPL1 protein. Homo sapiens (Human) Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID-9606; [1]  SEQUENCE FROM N.A. |
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| A.  O01) to the EMBL/GenBank/DDBJ databases.  AAH11904.1;  F:O-sialoglycoprotein endopeptidase activity; IEA.  F:zinc ion binding; IEA.  P:proteolysis and peptidolysis; IEA.  905; Peptidase M22; 180; Pept M22 Osialgl.  eptidase M22; 1.  OSIALOFTASE.  OSIALOFTASE.  OSIALOFTASE.  Peptidase M22; 1.  329; 9cp; 1.  329; 9cp; 1. | le; 88257; PubMed=12477932; DOI=10.1073/pnas.242603899; R.L., Feingold E.A., Grouse L.H., Derge J.G., D., COllins F.S., Wagner L., Shenmen C.M., Schuler G.D., F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Coquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Wchan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., elton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., W., Touchman J.W., Green E.D., Dickson M.C., C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., and initial analysis of more than 15,000 full-length human DNA sequences."; acad. Sci. U.S.A. 99:16899-16903(2002). | ARY; PRT; 414 AA. el. 19, Created) el. 19, Last sequence update) el. 26, Last annotation update) chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.                                                         |

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Li Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

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RC STRAIN=CZECH II; TISSUB=Mammary tumor;

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RX Altacher R.D., Collins F.S., Wagner L.M., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordal M.S., Carninci G.M., Hong L.,

RA Hopkins R.F., Joshiyuki S., Carninci P., Prange C.,

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RA Willalon A., and initial analysis of more than 15.000 full-length human

"Generation and initial analysis of more than 15.000 full-length human

"Generation and initial analysis of more than 15.000 full-length human
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R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

R InterPro; IPR00905; Peptidase M22;

R InterPro; IPR009180; Peptidase M22; I.

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R PIRSF; PIGSP098; OSIALOPTASE.

R PINSF; PIGR098; OSIALOPTASE.

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Carninci P., Hayashizaki Y.;

"High-efficiency full-length cDNA cloning.";

Meth. Enzymol. 303:19-44(1999).
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Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
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Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
enriched library, clone:B230219017 product:similar to PUTATIVE
  Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new gegenome Res. 10:1617-1630(2000).
  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
  STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
   "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
   "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
[3]
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. 10:1757-1771(2000).
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  2
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   annotation
   Team;
   genes.";
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   01-MAR-2004 (TrEMBLrel. 17, Last sequence update)
Mus musculus 10 days embryo whole body cDNA, RIKEN
enriched library, clone:2610001M19 product:similar t
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STRAIN-C578L/63; TISSUE-Whole body;

MEDLINE-99279253; PubMed=10349636; DOI=10.10

Carninci P., Hayashizaki Y.;

"High-efficiency full-length cDNA cloning.";

Meth. Enzymol. 303:19-44(1999).
  Mame=Osgepl1;
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata;
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   Adāchi J., Aizāwa K., Akimura T., Arakāwa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hirozane T., Imozane T., Imozane T., Imozane T., Imozane T., Imozane T., Imozane T., Imozane T., Kagawa I., Kasukawa T., Kori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojina Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami Tagawa A., Takahashi F., Takaku-Akahira S., Takada Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
   01-JUN-2001
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RC STRAIN=C55BL/6J; TISSUE=Whole body;

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RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carrinci P.,

RA KOnno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Yoneda Y., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

UN 16]
  STRAIN-C57BL/6J; TISSUE-Whole body;

A Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

A Adachi J., Aizawa K., Akahira S., Akimura T., Fukunishi Y., Furuno M.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

A Imotani K., Ishii Y., Itoh M., Izawa M., Koya S., Kurihara C.,

A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

Kawai J., Kojima Y., Konno H., Nishi K., Nomura K., Numazaki R., Ohno M.,

A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

A Okazaki Y., Okido T., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Tokhahashi P., Tanaka T.,

A Tejima Y., Toya T., Yasumira T., Yasumishi A., Yoshida K., Yoshino M.,

A Muramatsu M., Hayashizaki Y.;

Bubmitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
   MEROPS; M22.004; -...

R MGD; MGI:1919335; Osgepl1.

R GO; GO:0008450; F:O-sialoglycoprotein endopeptidase activity; IEA.

R GO; GO:000823; F:peptidase activity; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramateu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
   The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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  Nature 409:685-690(2001).
  "Functional annotation of a full-length mouse cDNA collection.";
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R EMBL; BC078974; AAH78974.1; -.

R GO; GO:0008450; F:C-sialoglycoprotein endopeptidase activity; IEA

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R GO; GO:0008508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR00905; Peptidase M22.

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RC TISUE-Testis;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Kax S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,

RA Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Wedin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,

RA Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RA Willalon D.K., Muzny D.M., Sodergren E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Korywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Korenes S.J., Marra M.A..
   With the sequences."; of more than 15,000 and mouse cDNA sequences."; natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
  25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
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   Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
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  Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarrin H., Li P., Liao G., Miranda A., Mungall C. Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wa Yu C., Lewis S.E., Rubin G.M., Celniker S.;
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   MEDLINE=22426069; PubMed=12537572;
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        SEQUENCE FROM N.A.

TISSUB-Floral meristem 5-10 days when regenerated in vitr Fan J.H., Ma Y., Zhang X.S.;
Fan J.H., Ma Y., Zhang X.S.;
"Hyacinthus orientalis O-sialoglycoprotein endopeptidase mRNA, expressed during regeneration of floral bud.";
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY389554; AA708652.1; -.
InterPro; IPR000905; Peptidase_M22.
  Protease.
SEQUENCE
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GO; GO:0008270; F:zinc ion binding; IEA.

GO; GO:0008270; F:zinc ion binding; IEA.

GO; GO:0008270; F:zinc ion binding; IEA.

InterPro; IPR0009065; Peptidase and peptidolysis; IEA.

InterPro; IPR009180; Peptidase M22 Osialgl.

Pfam; PF00814; Peptidase M22; I.

PIRSF; PIRSF004537; Osialglc pptds; 1.
   Hyacinthus orientalis.
Eukaryota; Viridiplantae; Str.
Spermatophyta; Magnoliophyta;
   25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation updat
25-OCT-2004 (TrEMBLrel. 28, Last annotation updat
0-sialoglycoprotein endopeptidase (Fragment).
  EMBL; AC002387; AAB82636.2; -. EMBL; AY024338; AAK00530.1; -. EMBL; AY063864; AAL36220.1; -. EMBL; AY117283; AAM51358.1; -.
   Theologis A.;
Submitted (JUN-2002) to the
  Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lir
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T.,
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W.,
  Q677H2;
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PR00789; OSIALOPTASE.
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   LVCPPPSLCTDNGVMVAWTGLEHFRVG-----
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PD002367; Peptidase\_M22; 1.

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  MEDILINE=1136507; PubMed=11481430; DOI=10.1073/pnas.161294398;

A Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

B Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,

Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,

Pohl T., Portetelle D., Puehler A., Purnelle B., Ramaperger U.,

R Pohl T., Portetelle D., Vandenbol M., Weidner S., Galibert F.;

"Analysis of the chromosome sequence of the legume symbiont

Sinorhizobium meliloti strain 1021.";

Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

R PRESI, AL591792; CAC47657.1; -.

R GO; GO:00016787; F:hydrolase activity; IEA.

GO; GO:0008450; F:O-sialoglycoprotein endopeptidase activity; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

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Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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Q1-MAR-2004 (TrEMBLRel. 26, Last annotation update)
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PIRSF; PIRSF004537; Osialglc pptds; 1.

PRINTS; PR00789; OSIALOPTASE.

ProDom; PD002367; Peptidase M22; 1.

TIGRPAMs; TIGR00329; gcp; 1.

Complete proteome; Hydrolase.

SEQUENCE 360 AA; 37906 MW; A07F946AB562EA86 CRC64;
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  14 LGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKN
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  IGTTIDDAIGEAYDKTARWLGL----DMGKGGGPALEELALEGDANSVKFKIPWRQHKD
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145 LILVKGVGEYERWGTTIDDÅLGEAFDKTÄKLLGL-PYP-----GGPÄVERAAQAGNAER 197

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